

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-1

Query Match 99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRGLPINQRFILVEL 62
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Db 123 YDRLEQLAGNLRNIELGNPLEEASALYYSTGCTQPTLARSFIICQMISEAARFQ 182
QY 183 YIEGEMRTRIRYNRRS 198
Db 183 YIEGEMRTRIRYNRRS 198

RESULT 9
US-08-646-360-1

;; Sequence 1, Application US/08646360
;; Patent No. 5837491
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-646-360-1
Query Match 99.1%; Score 1010; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRGLPINQRFILVEL 62
QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLPTDVQNYTFAFGN 122
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLPTDVQNYTFAFGN 122
QY 123 YDRLEQLAGNLRNIELGNPLEEASALYYSTGCTQPTLARSFIICQMISEAARFQ 182
Db 123 YDRLEQLAGNLRNIELGNPLEEASALYYSTGCTQPTLARSFIICQMISEAARFQ 182
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Db 183 YIEGEMTRIRYNRRS 198
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RESULT 10
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-1

Query Match 99.1%; Score 1010; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
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Db 63 SNHAELSVTLALDVTNAYVYVGRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTTAFGNN 122

QY 123 YDRLEQIAGNLRENIEIENGPLEEASIALYXXYSTGGTOLPTLARSTICIMISEARFQ 182
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QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198
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RESULT 11
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCI/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-1

Query Match 99.1%; Score 1010; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRGLPINQRFILVEL 62
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Db 123 YDRLEQAGNLRNIELGNPLEEASALYYVSTGGTQPLTLARSFIICQMISEAARFQ 182
QY 183 YIEGEMRTIRYNRRS 198
Db 183 YIEGEMRTIRYNRRS 198
RESULT 12
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-1
Query Match 99.1%; Score 1010; DB 4; Length 267;
Best Local Similarity 100.0%; Fred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRGLPINQRFILVEL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRGLPINQRFILVEL 62
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Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNYTFAFGN 122
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Db 123 YDRLEQAGNLRNIELGNPLEEASALYYVSTGGTQPLTLARSFIICQMISEAARFQ 182
QY 183 YIEGEMRTIRYNRRS 198
Db 183 YIEGEMRTIRYNRRS 198
RESULT 13
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1

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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
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QY 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICQMISEAARFQ 182
Db 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICQMISEAARFQ 182
QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198

RESULT 14
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biotynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-8
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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 124 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICQMISEAARFQ 183
QY 183 YIEGEMTRIRYNRRS 198
Db 184 YIEGEMTRIRYNRRS 199

RESULT 15
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/378,761A
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-27

Query Match          99.1%; Score 1010; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.7e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	207	YIEGEMRTRIRYNRRS	222

Search completed: February 10, 2004, 16:29:33
Job time : 12.4485 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 25.5389 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-7
Perfect score: 1019
Sequence: 1 MYPKQYPIINTTAGATVQS.....ARFQVIEGEMTRIRYNRRS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1019	100.0	198	12	US-10-083-336A-7
2	1019	100.0	267	12	US-10-083-336A-7
3	1019	100.0	267	12	US-10-282-935-1
4	1010	99.1	198	12	US-10-440-796-1
5	1010	99.1	199	12	US-10-083-336A-3
6	1010	99.1	200	12	US-10-083-336A-5
7	1010	99.1	267	12	US-10-083-336A-10
8	1010	99.1	267	12	US-10-127-890-1
9	950	92.3	188	12	US-10-083-336A-8
10	941	92.3	188	12	US-10-083-336A-4
11	941	92.3	189	12	US-10-083-336A-6
12	941	92.3	190	12	US-10-083-336A-11
13	924.5	90.7	185	12	US-10-083-336A-9
14	738	72.4	179	12	US-10-083-336A-2
15	342	33.6	247	10	US-09-792-793A-39

16	342	33.6	247	12	US-10-127-890-6
17	342	33.6	247	12	US-10-375-209A-39
18	342	33.6	289	12	US-10-280-679B-4
19	323.5	31.7	251	12	US-10-282-935-3
20	323.5	31.7	251	12	US-10-440-796-3
21	312	30.6	247	10	US-09-792-793A-34
22	312	30.6	247	12	US-10-375-209A-34
23	277	27.4	263	12	US-10-127-890-4
24	277	27.2	263	12	US-10-127-890-7
25	276	27.1	252	9	US-09-347-064-2
26	276	27.1	252	9	US-09-347-064-8
27	267.5	26.3	248	12	US-10-127-890-5
28	246.5	24.2	251	12	US-10-127-890-110
29	246.5	24.2	251	12	US-10-127-890-111
30	245.5	24.1	251	12	US-10-127-890-101
31	244.5	24.0	251	12	US-10-127-890-99
32	244.5	24.0	251	12	US-10-127-890-107
33	243.5	23.9	251	12	US-10-127-890-100
34	243.5	23.9	251	12	US-10-127-890-106
35	242.5	23.8	251	9	US-09-765-527-247
36	242.5	23.8	251	12	US-10-127-890-2
37	242.5	23.8	251	12	US-10-127-890-102
38	242.5	23.8	251	12	US-10-127-890-103
39	242.5	23.8	251	12	US-10-127-890-104
40	242.5	23.8	251	12	US-10-127-890-105
41	242.5	23.8	316	12	US-10-074-596-1
42	242.5	23.8	507	12	US-10-074-596-11
43	241.5	23.7	251	12	US-10-127-890-109
44	241.5	23.7	293	9	US-09-765-527-259
45	241.5	23.7	309	9	US-09-765-527-253

ALIGNMENTS

RESULT 1

US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US2003018166SAI
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match	100.0%	Score 1019;	DB 12;	Length 198;
Best Local Similarity	100.0%;	Pred. No. 1.4e-108;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MYPKQYPIINTTAGATVQSYTNFTIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFTILV	60	
Db	1	MYPKQYPIINTTAGATVQSYTNFTIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFTILV	60	
Qy	61	ELSNHAEISVTIALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAIHTLFTDVQNRVTFAPG	120	
Db	61	ELSNHAEISVTIALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAIHTLFTDVQNRVTFAPG	120	
Qy	121	GNYDLEQLAGNLRNIEIENGPLEEASALYYSTGTGQTLPRLARSFIICIMISEAR	180	
Db	121	GNYDLEQLAGNLRNIEIENGPLEEASALYYSTGTGQTLPRLARSFIICIMISEAR	180	
Qy	181	FQYIEGEMTRIRYNRRS	198	

RESULT 5

US-10-083-336A-5

; Sequence 5, Application US/10083336A
 ; Publication No. US20030181665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-5

Query Match 99.1%; Score 1010; DB 12; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.5e-107;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 DB 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63

QY 63 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
 DB 64 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123

QY 123 YDRLEQLAGNLRENIELGNPLEEAISSALYYSTGTQTLPTLARSFFIICMISSAARFQ 182
 DB 124 YDRLEQLAGNLRENIELGNPLEEAISSALYYSTGTQTLPTLARSFFIICMISSAARFQ 183

QY 183 YIEGEMTRIRYNRRS 198
 DB 184 YIEGEMTRIRYNRRS 199

RESULT 6

US-10-083-336A-10

; Sequence 10, Application US/10083336A
 ; Publication No. US20030181665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 200
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-10

Query Match 99.1%; Score 1010; DB 12; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.6e-107;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 DB 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63

QY 63 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

DB 64 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123

QY 123 YDRLEQLAGNLRENIELGNPLEEAISSALYYSTGTQTLPTLARSFFIICMISSAARFQ 182

DB 124 YDRLEQLAGNLRENIELGNPLEEAISSALYYSTGTQTLPTLARSFFIICMISSAARFQ 183

QY 183 YIEGEMTRIRYNRRS 198

DB 184 YIEGEMTRIRYNRRS 199

RESULT 7

US-10-127-890-1

; Sequence 1, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; Proteins

NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELE: 650 388-1248

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 99.1%; Score 1010; DB 12; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.4e-107;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62

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Db      3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
QY      63 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
Db      63 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
QY      123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 182
Db      123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 182
QY      183 YIEGEMTRIRYNRRS 198
Db      183 YIEGEMTRIRYNRRS 198

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RESULT 8

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US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

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Query Match      99.1%; Score 1010; DB 12; Length 576;
Best Local Similarity 100.0%; Pred. No. 7.1e-107;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
Db      38 PKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVEL 97
QY      63 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
Db      98 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 157
QY      123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 182
Db      158 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 217
QY      183 YIEGEMTRIRYNRRS 198
Db      218 YIEGEMTRIRYNRRS 233

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RESULT 9

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US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

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Query Match      93.2%; Score 950; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 1.1e-100;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY      1 MVEPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILV 60
Db      1 MVEPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILV 50
QY      61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 120
Db      51 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 110
QY      121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAAR 180
Db      111 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAAR 170
QY      181 YIEGEMTRIRYNRRS 198
Db      171 YIEGEMTRIRYNRRS 188

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RESULT 10

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US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

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Query Match      92.3%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY      3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
Db      3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVEL 52
QY      63 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
Db      53 SNEHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 112
QY      123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 182
Db      113 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQTLPLARSFFIICIMISEAARFQ 172
QY      183 YIEGEMTRIRYNRRS 198
Db      173 YIEGEMTRIRYNRRS 188

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RESULT 11

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US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1

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; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match          92.3%; Score 941; DB 12; Length 189;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILVEL 62
Db 4 PQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 53

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 122
Db 54 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 113

QY 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 182
Db 114 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 173

QY 183 YIEGEMTRIRYNRRS 198
Db 174 YIEGEMTRIRYNRRS 189

RESULT 12
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match          92.3%; Score 941; DB 12; Length 190;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILVEL 62
Db 4 PQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 53

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 122
Db 54 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 113

QY 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 182
Db 114 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 173

QY 183 YIEGEMTRIRYNRRS 198
Db 174 YIEGEMTRIRYNRRS 189

RESULT 13
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match          90.7%; Score 924.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 9e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 PQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILVEL 62
Db 3 PQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILVEL 49

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 122
Db 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 109

QY 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 182
Db 110 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQMISEARFQ 169

QY 183 YIEGEMTRIRYNRRS 198
Db 170 YIEGEMTRIRYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match          72.4%; Score 738; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.2e-76;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: February 10, 2004, 16:53:53
Job time : 25.5389 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.7146 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019

Sequence: 1 MVPKQYPIINFTTAGATVQS.....ARFOYIEGEMRTIRVYRRS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1010	99.1	576	1 RLCSA	ricin D precursor
2	920.5	90.3	564	1 RLCSA	agglutinin precursor
3	353.5	34.7	528	2 S2431	abrin-d precursor
4	353.5	34.7	562	2 S16022	abrin-c precursor
5	345	33.9	527	2 S32430	abrin-b precursor
6	342	33.6	289	1 RLTTZ	rRNA N-glycosidase
7	338	33.2	247	2 JUT0393	karasurin - Mongol
8	338	33.2	247	2 JCS032	karasurin-B - Tric
9	338	33.2	289	2 JCS066	karasurin C - Tric
10	336.5	33.0	251	2 S39761	abrin (clone 7.2)
11	329.5	32.3	528	1 TLISA	abrin-a precursor
12	307.5	30.2	278	2 S23119	beta-luffin - smoo
13	300.5	29.5	250	2 JN0108	luffin-b - smoo
14	291	28.6	570	2 S62627	agglutinin I precu
15	286	28.1	254	2 PD0018	miscleoe lectin I
16	284.5	27.9	277	2 S24494	rRNA N-glycosidase
17	281	27.6	286	2 S25560	rRNA N-glycosidase
18	278	27.3	245	2 JC4840	rRNA N-glycosidase
19	277	27.2	286	1 RLPUGG	rRNA N-glycosidase
20	274	26.9	286	2 JC4235	rRNA N-glycosidase
21	242.5	23.8	316	2 JT0753	rRNA N-glycosidase
22	197.5	19.4	294	2 S28421	rRNA N-glycosidase
23	182	17.9	313	2 S17757	rRNA N-glycosidase
24	180.5	17.7	261	2 JE0401	antiviral protein
25	178	17.5	278	2 A39817	rRNA N-glycosidase
26	156	15.3	272	2 JC4811	betavulgin - beet
27	149.5	14.7	289	2 TL2573	rRNA N-glycosidase
28	140	13.7	280	1 RLBH	rRNA N-glycosidase
29	137	13.4	275	2 S33631	trititin - wheat

ALIGNMENTS

RESULT 1

RLCSA

ricin D precursor - castor bean

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Ricinus communis (castor bean)

C>Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text change 16-Jul-1999

C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Jadin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A:Reference number: A24041; MUID:86067214; PMID:2999712

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <HAL>

A:Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R:Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A:Reference number: S20513; MUID:92163016; PMID:1371405

A:Accession: S20513

A:Molecule type: DNA

A:Residues: 1-576 <TRE>

A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A:Title: Nucleotide sequence of cloned cDNA coding for prepropricin.

A:Reference number: A24614; MUID:85179479; PMID:3838723

A:Accession: A24614

A:Molecule type: mRNA

A:Residues: 12-75 'D', 77-550, 'R', 552-576 <LAM>

A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R:Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile

A:Reference number: A03372

A:Accession: A03372

A:Molecule type: protein

A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A:Note: this paper cites the others in the series providing experimental details for the

R:Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010

A:Accession: A24010

A:Molecule type: protein

A:Residues: 315-383, 'PS', 386-576 <ARA>

R:Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A:Title: Primary structure of Ala chain of ricin D.

A:Reference number: A03374

A:Accession: A03374

A:Molecule type: protein

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',405-527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'P' <FUN>
 A;Note: This paper, on one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action.
 A;Reference number: A48237; MUID:91352006; PMID:1881893
 A;Contents: annotation; active site
 R;Robertus, J.D.
 Proteins 10, 260-269, 1991
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
 A;Reference number: A48238; MUID:91352005; PMID:1881892
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
 Proteins 10, 251-259, 1991
 A;Title: Structure of ricin A-chain at 2.5 angstroms.
 A;Reference number: A48239; MUID:91352004; PMID:1881891
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain; B chains are also responsible for cell agglutination (lectin).
 C;Comment: This protein is cytotoxic and very poisonous to animals.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-35/Domain: signal sequence #status predicted <SIG>
 F;36-302/Product: ricin D chain A #status experimental <ACH>
 F;46-293/Domain: rRNA N-glycosidase homology <RNG>
 F;315-576/Product: ricin D chain B #status experimental <BCH>
 F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
 F;45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;212/Active site: Glu #status experimental
 F;215/Active site: Arg #status predicted
 F;294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
 F;336,349,360/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status experimental
 F;548,569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match 99.1%; Score 1010; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 3.6e-93;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PKQYPIINFAGTAGVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 62
 Db 38 PKQYPIINFAGTAGVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 97

Qy 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGN 122
 Db 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGN 157

Qy 123 YDRLEQLAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 182
 Db 158 YDRLEQLAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 217

Qy 183 YIEGEMTRIRYNRRS 198
 Db 218 YIEGEMTRIRYNRRS 233

RESULT 2
 RLCSAG
 agglutinin precursor - castor bean
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Ricinus communis (castor bean)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A24261; A24210
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
 J. Biol. Chem. 260, 15682-15686, 1995
 A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
 A;Reference number: A24261; MUID:86059449; PMID:2999130
 A;Accession: A24261
 A;Molecule type: mRNA
 A;Residues: 1-564 <ROB>
 A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
 Biochim. Biophys. Acta 872, 277-285, 1996
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 A;Reference number: A24210
 A;Accession: A24210
 A;Molecule type: protein
 A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-574,'E',575-584,'W',586-590,'LI',593-594,'P' <FUN>
 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-290/Product: agglutinin chain A #status predicted <ACH>
 F;35-281/Domain: rRNA N-glycosidase homology <RNG>
 F;303-564/Product: agglutinin chain B #status experimental <BCH>
 F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
 F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;200,203/Active site: Glu, Arg #status predicted
 F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
 F;324,337,348/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status predicted
 F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;536,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 90.3%; Score 920.5; DB 1; Length 564;
 Best Local Similarity 91.8%; Pred. No. 4.1e-75;
 Matches 180; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 3 PKQYPIINFAGTAGVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 62
 Db 27 PKQYPIINFAGTAGVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 86

Qy 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGN 122
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGN 146

Qy 123 YDRLEQLAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 182
 Db 147 YDRLEQLAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 205

Qy 183 YIEGEMTRIRYNRRS 198
 Db 206 YIEGEMTRIRYNRRS 221

RESULT 3
 S32431
 abrin-d precursor - Indian licorice (fragment)
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Abrus precatorius (Indian licorice)
 C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
 C;Accession: S32431; S34408
 E;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing. Co
 A;Reference number: S32429; MUID:93132798; PMID:8421133
 A;Accession: S32431
 A;Molecule type: mRNA
 A;Residues: 1-528 <HUN>
 A;Cross-references: GB:M98346
 R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
 submitted to the EMBL Data Library, March 1993
 A;Reference number: S34408
 A;Accession: S34408
 A;Molecule type: mRNA
 A;Residues: 1-169,'C',171-320,'L',322-528 <HU2>
 A;Cross-references: GB:M98346
 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxic
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
 F;1-251/Product: abrin-d chain A #status predicted <ACH>
 F;7-246/Domain: rRNA N-glycosidase homology <RNG>
 F;261-528/Product: abrin-d chain B #status predicted <BCH>

F:283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted
 F:200,253,361,401,402/Binding site: carbohydurate (Asn) (covalent) #status predicted
 F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 F:288,312/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
 F:500,521/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 34.7%; Score 353.5; DB 2; Length 528;
 Best Local Similarity 45.5%; Pred. No. 5e-24;
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILVELSN 64
 Db 1 QDQVKEFTTEGATSQSYKQFTEALRQLTGG--LIHDPVLPDPPTVEERNRYITVELSN 58
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVTFAGGNYD 124
 Db 59 SERESIEGIDVNTAYVVGVRAGNSQSYFL--RDAPASASTYLPFGTQ-RYSLRFDGSYG 114
 Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 115 DLERWAHQTRREISIGLQALTHAIS---FLRSGASNDEKARTLIVIQMASEARVRYI 171
 Qy 185 EGEWTRIR 193
 Db 172 SNRVGVSR 180

RESULT 4

SL16022
 abrin-c precursor - Indian licorice
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S16022
 R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
 Eur. J. Biochem. 198, 723-732, 1991
 A:Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chain
 A:Reference number: S16022; MUID:91266957; PMID:2050149
 A:Accession: S16022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-562 <WOO>
 A:Cross-references: EMBL:X55667; NID:gl6084; PIDN:CAA39202.1; PID:G16085
 C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
 The A and B chains are linked by a single disulfide bond, which is essential for toxicity
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
 F:35-285/Product: abrin-c chain A #status predicted <ACH>
 F:41-280/Domain: rRNA N-glycosidase homology <RNG>
 F:295-562/Product: abrin-c chain B #status predicted <BCH>
 F:317-359,360-400,403-441,448-483,487-526,528-562/Region: 40-residue repeats
 F:35/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:198,201/Active site: Glu, Arg #status predicted
 F:234,287,395,435,436/Binding site: carbohydurate (Asn) (covalent) #status predicted
 F:281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
 F:322,346/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
 F:534,555/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 34.7%; Score 353.5; DB 2; Length 562;
 Best Local Similarity 45.5%; Pred. No. 5.4e-24;
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILVELSN 64
 Db 35 QDQVKEFTTEGATSQSYKQFTEALRQLTGG--LIHDPVLPDPPTVEERNRYITVELSN 92
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVTFAGGNYD 124
 Db 93 SERESIEGIDVNTAYVVGVRAGNSQSYFL--RDAPASASTYLPFGTQ-RYSLRFDGSYG 148

Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 149 DLERWAHQTRREISIGLQALTHAIS---FLRSGASNDEKARTLIVIQMASEARVRYI 205
 Qy 185 EGEWTRIR 193
 Db 206 SNRVGVSR 214

RESULT 5

S32430
 abrin-b precursor - Indian licorice (fragment)
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 C:Accession: S32430; JCI399
 R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A:Title: Primary structure of three distinct isoabrin determined by cDNA sequencing. Cor
 A:Reference number: S32429; MUID:93132798; PMID:8421313
 A:Accession: S32430
 A:Molecule type: mRNA
 A:Residues: 1-527 <HUN>
 A:Cross-references: GB:M98345; NID:gl66296; PIDN:AAA32625.1; PID:gl66297
 R:Kimura, M.; Sumizawa, T.; Funatsu, G.
 Biosci. Biotechnol. Biochem. 57, 166-169, 1993
 A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
 A:Reference number: JCI398; MUID:93169023; PMID:7763422
 A:Accession: JCI399

A:Molecule type: protein
 A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
 A:Experimental source: seed
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; py
 F:1-250/Product: abrin-b chain A #status predicted <ACH>
 F:7-245/Domain: rRNA N-glycosidase homology <RNG>
 F:260-527/Product: abrin-b chain B #status experimental <BCH>
 F:282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:110,360,400/Binding site: carbohydurate (Asn) (covalent) #status predicted
 F:163,166/Active site: Glu, Arg #status predicted
 F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
 F:287,311/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
 F:499,520/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 33.9%; Score 345; DB 2; Length 527;
 Best Local Similarity 45.5%; Pred. No. 2.9e-23;

Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;
 Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILVELSN 64
 Db 1 QDQVKEFTTEGATSQSYKQFTEALRQLTGG--LIHDPVLPDPPTVEERNRYITVELSN 58
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVTFAGGNYD 124
 Db 59 SDTESIEAGIDVNTAYVVGVRAGNSYFL--RDAPTSAGRYLFTGTQ-QYSLRFGSYI 114
 Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 115 DLERLAQTRQQLPLGLQALRHAISFL----QSGTDDQETARTLIVIQMASEARVRYI 170
 Qy 185 EGEWTRIRYN 195
 Db 171 SYRVGVSR 181

RESULT 6

RLT2T
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian sr
 N:Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)

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Best Local Similarity 39.5%; Pred.No. 2.5e-23;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;

QY 9 INFTTAGATVQSYTNPIRAVRGRLTTGADVREHPVLNPRVGLPINORFILVELSNHAEL 68
   : : ||| || : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 25 VSRFLSGATSSSYGVFISNLRKALPERKL-YDIPLL--RSLPGSQRYALHILHTNYADE 81
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 82 TISVAIDVTNVINGVRAGTGYFF--NEASATEAAKYVFKDAWKVTLPSYSGNYERLQ 138
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 128 QLAGNLRNTELGNGPLEEPAISALYYSTGGTQLPTLARSFFICIMISEARFOYIEGE 187
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 139 TAAGKIRENIPGLPALDSAITTLFYNN-----SAASALMWLTQSTSEAAKYKFFIEQ 193
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 188 MRTRI 192
   : : : :
Db 194 IGRKV 198
   : : : :

RESULT 7
JUC0393
Karasurin - Mongolian snake-gourd
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C:Accession: JUC0393; PS0163
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
Chem. Pharm. Bull. 39, 1244-1249, 1991
A:Title: The complete amino acid sequence of an abortifacient protein, karasurin
A:Reference number: JUC0393; MUID:92005921; PMID:1914000
A:Accession: JUC0393
A:Molecule type: protein
A:Residues: 1-247 <TOY>
A:Note: a sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient
C:Keywords: Domain: rRNA N-glycosidase homology <RNG>

Query Match 33.2%; Score 338; DB 2; Length 247;
Best Local Similarity 40.0%; Pred.No. 4.7e-23;
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

QY 9 INFTTAGATVQSYTNPIRAVRGRLTTGADVREHPVLNPRVGLPINORFILVELSNHAEL 68
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 2 VSRFLSGATSSSYGVFISNLRKALPERKL-YDIPLL--RSLPGSQRYALHILHTNYADE 58
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 59 TISVAIDVTNVVGVRAGTGYFF--NEASATEAAKYVFKDAWKVTLPSYSGNYERLQ 115
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 128 QLAGNLRNTELGNGPLEEPAISALYYSTGGTQLPTLARSFFICIMISEARFOYIEGE 187
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 116 TAAGKIRENIPGLPALDSAITTLFYNN-----SAASALMWLTQSTSEAAKYKFFIEQ 170
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 188 MRTRI 192
   : : : :
Db 171 IGRKV 175
   : : : :

RESULT 8
JUC5032
karasurin-B - Trichosanthes kirilowii var. japonica
C:Species: Trichosanthes kirilowii var. japonica
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C:Accession: JUC5032
C:Superfamily: Amino acid sequences and ribosome-inactivating activities of karasurin
Biol. Pharm. Bull. 19, 1485-1489, 1996
A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin
A:Reference number: JUC5032; MUID:97108848; PMID:8951169
A:Accession: JUC5032
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-247 <KON>

```

Query Match	33.2%	Score	338;	DB	2;	Length	289;
Best Local Similarity	40.0%;	Pred.	No. 5-7e-23;				
Matches	74;	Conservative	46;	Mismatches	53;	Indels	12; Gaps
							5;
QY	9	INFTTAGATVGSYNFTRAVRGRLLTGADVDRHEPVLPNRVGLPEINORFILVELSNHAEL	68				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Db	25	VSRFLSGATSSGYGVTISNRKALPYEKL--YDIPLL--RSTLPGSQRYALHILNTYADE	81				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
QY	69	SVTIALDVNAYVVGYRAGNSAYFFHPDNQEDA-EATHLETDVNRYTFAFGNYDRLE	127				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Db	82	TISVAIDVTNVVMGYRAGDTSYFF--NEASATEAKYVFCDARKVVLPFYSGNYERLQ	138				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
QY	128	QLAGNLRENIELNGPLPEALSAIYYVGTQTLPLEARSLFIICIMISEAARFOYTEGE	187				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Db	139	IARGKIRENIPLGLPALDSAITLTIFYNN-----SAA\$AMWLIQSTSEAAKYKFIEQQ	193				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
QY	188	METRI	192				

K/Furukawa, S.; Taguchi, T.; Kametani, S. *Aggr. Biol. Chem.* 52: 1095-1097. 1988

QY 9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLNPRVGLPINQREILVELSNHAEL 68
Db 5 IXFTEGATQSQYKQFIEALRRLRG--LIHDIPLVDPPTTLOEKNRVITVELSNSDTE 62
QY 69 SVTLALDVTNAVVGVRAGNSAYFFH--PDNCEDEAETHLFTDVQNRVYTFAGGNYDRLL 126
Db 63 STEVGIDVTNAVVRAGTQSYFLEADPSSAD-----YLFTGT-DQHSLPFYGYGDLL 116
QY 127 EQLAGNLRNIEIENGPLEBEASALYYSTGTGTQPTLARSFIIICIMISEAARFQYIEG 186
Db 117 ERWAHOSRQIPLGLQALTHGIS---FFRSGGNDNEKARTLIVTIQWAAEARFYISN 173
QY 187 EMRTRIR 193
Db 174 RVRVSIQ 180

RESULT 12
S23519
beta-luffin - smooth loofah
C:Species: Luffa cylindrica (smooth loofah)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C:Accession: S23519; S23113
R:Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 19, 887-889, 1992
A:Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
A:Reference number: S23519; MUID:92353400; PMID:1643290
A:Accession: S23519
A:Molecule type: mRNA
A:Residues: 1-278 <RNG>
A:Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:26-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match 30.2%; Score 307.5; DB 2; Length 278;
Best Local Similarity 35.8%; Pred.No.3.1e-20;
Matches 67; Conservative 45; Mismatches 64; Indels 11; Gaps 3;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLNPRVGLPINQREILVELSNHAEL 68
Db 24 VPSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRVILMQLSNVDK 80
QY 69 SVTLALDVTNAVVGVRAGNSAYFFHDPDNCDEAETHLFTDVQNRVYTFAGGNYDRLEQ 128
Db 81 AITMAIDVTNVITMGVLVNSTSYFF---NESDAKLASQVYFKGSTIVTLFYSNGYERLQN 137
QY 129 LAGNLRNIEIENGPLEEASALYYSTGTGTQPTLARSFIIICIMISEAARFQYIEGEM 188
Db 138 AAGVKREKIPLGFRAFDSAITSLFHYDS-----TAAAGAFVLIIQTAAERFKYIEGQI 192
QY 189 RTRIRVN 195
Db 193 IERIPKN 199

RESULT 13
JN0108
luffin-b - smooth loofah
C:Species: Luffa cylindrica (smooth loofah)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
C:Accession: JN0108
R:Islam, M.R.; Hirayama, H.; Funatsu, G.
Agric. Biol. Chem. 55, 229-238, 1991
A:Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from
A:Reference number: JN0108; MUID:91248488; PMID:1368666
A:Accession: JN0108
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-250 <ISL>
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:5-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 29.5%; Score 300.5; DB 2; Length 250;

Best Local Similarity 34.2%; Pred. No. 1.1e-19;
Matches 64; Conservative 48; Mismatches 64; Indels 11; Gaps 3;
QY 9 INFNTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILVELSNHAEL 68
DB 3 VSFSLSGADSKSYKFTALRKALPKSEKVNIPULLPSAGA-----SRYILMQLSNYDAK 59
QY 69 SVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 128
DB 60 AITMAIDVTNVIMGYLVNSYF---ANESAKLASQVVFKGSLVTIPYSGNYERLQN 116
QY 129 LAGNLRNIEIENGPLEAISALYYSTGCTQPLTARSFIIICIQMISEAARFQVIEGEM 188
DB 117 AAGTKREKIPGLFRALDSALTSIFHYDS-----TAAAAAFVLQTTAAEASRFXIEGQI 171
QY 189 RTRIRYN 195
DB 172 IERIPKN 178
RESULT 14
S62627
agglutinin I precursor - European elder
C:Species: Sambucus nigra (European elder)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S62627; S62619
R:van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Eur. J. Biochem. 235, 128-137, 1996
A:Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; MUID:96202926; PMID:8631319
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VAN>
A:Cross-references: EMBL:U27122; NID:g1141772; PID:RAC49158.1; PID:g1141773
A:Accession: S62619
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-39;309-319 <VA2>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:37-283/Domain: rRNA N-glycosidase homology <RNG>
Query Match 28.6%; Score 291; DB 2; Length 570;
Best Local Similarity 39.0%; Pred. No. 2.4e-18;
Matches 76; Conservative 33; Mismatches 74; Indels 12; Gaps 6;
QY 1 MVPKQVPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILV 60
DB 29 VTPPVPSVSFNLTGA--DTIEFLRALQEKVILGNHTAFDLPVLPNPSQVSDSNREVLV 86
QY 61 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDN--QEDAEATHLFTDVQNRVYTF 118
DB 87 PLINPSGDTVTALDVVNLVAVPSSNGKSVFFSGSTAVQD-----NLFVDT-TQEELN 140
QY 119 FGGNYDRLEQAGNLRNIEIENGPLEAISALYYIS-TGCTQPLTARSFIIICIQMISE 177
DB 141 FTGNYTSLERQVGRVYIPLGPKSLDQAISSTYTLTAGDTKP-TARGLLVVVIQWSE 199
QY 178 AARFQYIEGEMTRI 192
DB 200 AARFRIELRIKTSI 214
RESULT 15
PD0018
mistletoe lectin I A chain - Viscum album (fragment)
C:Species: Viscum album
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C:Accession: PD0018
R:Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album
A:Reference number: PD0018; MUID:98308123; PMID:9642133

A:Accession: PD0018
A:Molecule type: protein
A:Residues: 1-254 <ESC>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
Query Match 28.1%; Score 286; DB 2; Length 254;
Best Local Similarity 38.4%; Pred. No. 2.4e-18;
Matches 81; Conservative 36; Mismatches 56; Indels 38; Gaps 10;
QY 13 TAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRVGLPIN--QRFILVELSNHAELSV 70
DB 9 THQTTGEEYRPFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNGQDSV 66
QY 71 TLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQLA 130
DB 67 TAAIDVTNAYVAVYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLFPNGSYPDLERYA 122
QY 131 GNLRNIEIENGPLEAISALYYSTGCTQPLTARSFIIICIQMISEAARF-----Q 182
DB 123 GH-RDQIEPLGIDQLIQSVTLARF---PGSTETQARSILILIQMISEAARFNPILWRVQ 178
QY 183 YIE-----GEMTRIRYN 195
DB 179 YINSGASFLPDVYVMLELETSMGQQSTQVQHS 209
Search completed: February 10, 2004, 16:28:02
Job time : 11.7146 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55 ; Search time 6.60489 Seconds
(without alignments)
1409.756 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019

Sequence: 1 MYPQYPIINFTTAGATVQS.....ARFOYIEGEMTRINYNRRS 198

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1010	99.1	576	1 RICI_RICCO	P02879 ricinus com
2	920.5	90.3	564	1 AGGL_RICCO	P06750 ricinus com
3	353.5	34.7	562	1 ABRC_ABRPR	P28590 abrus prec
4	345	33.9	527	1 ABRC_ABRPR	Q06077 abrus prec
5	342	33.6	289	1 RIPT_TRIKI	P09989 trichosan
6	341.5	33.5	282	1 RIPT_TRIKI	P98184 bryonia dio
7	338	33.2	289	1 RIPS_TRIKI	P24478 trichosan
8	330.5	32.4	563	1 NIGB_SAMNI	P33183 sambucus ni
9	329.5	32.3	528	1 ABRA_ABRPR	P11140 abrus prec
10	312	30.6	290	1 RIPI_BRYDI	P33185 bryonia dio
11	300.5	29.5	250	1 RIPI_BRYDI	P22851 luffa cylin
12	296.5	29.1	286	1 RIPI_CUCFI	Q9frx4 cucumis fig
13	286	28.1	254	1 MLIA_VISAL	P81446 viscum albu
14	284.5	27.9	277	1 RIPI_LUFY	Q00465 luffa cylin
15	281	27.6	286	1 RIPI_MOMCH	P29339 momordica b
16	277	27.2	286	1 RIPI_MOMCH	P16094 momordica c
17	260	25.5	294	1 RIPI_TRIAN	P56626 trichosan
18	242.5	23.8	316	1 RIPI_GELMU	P33186 gelonium mu
19	197.5	19.4	294	1 RIPI_PHYAM	Q03464 phytoacca
20	182	17.9	313	1 RIPI_PHYAM	P10297 phytoacca
21	180.5	17.7	261	1 RIPS_PHYAM	P23339 phytoacca
22	178	17.5	278	1 RIPI_MIRJA	P21326 mirabilis j
23	140	13.7	280	1 RIPI_HORVU	P04399 hordeum vul
24	133	13.1	280	1 RIPI_HORVU	P22444 hordeum vul
25	131	12.9	253	1 RIPT_SAPOF	Q41391 saponaria o
26	127	12.5	253	1 RIPT_SAPOF	Q41389 saponaria o
27	124	12.2	299	1 RIPI_SAPOF	P20656 saponaria o
28	123.5	12.1	293	1 RIPI_DIACA	P24476 dianthus ca
29	123	12.1	310	1 RIPI_PHYAM	Q40772 phytoacca
30	121	11.9	292	1 RIPI_SAPOF	P27559 saponaria o
31	111	10.9	319	1 SLTA_BP33	P09385 bacterioph
32	110	10.8	236	1 RIPI_SAPOF	P27560 saponaria o
33	107	10.5	300	1 RIPI_MAIZE	P25891 zea mays (m

RESULT 1

ID	RICI_RICCO	STANDARD;	PRT;	576 AA.
AC	P02879; P02880;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase)			
DE	(EC 3.2.2.22); Ricin B chain].			
OS	Ricinus communis (Castor bean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID=3988;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067214; PubMed=2999712;			
RA	Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,			
RA	Weaver R.F.;			
RT	"Genomic cloning and characterization of a ricin gene from Ricinus			
RT	communis."			
RL	Nucleic Acids Res. 13:8019-8033(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92163016; PubMed=1371405;			
RA	Tregear J.W., Roberts L.M.;			
RT	"The lectin gene family of Ricinus communis: cloning of a functional			
RT	ricin gene and three lectin pseudogenes."			
RL	Plant Mol. Biol. 18:515-525(1992).			
RN	[3]			
RP	SEQUENCE OF 12-576 FROM N.A.			
RX	MEDLINE=85179479; PubMed=3838723;			
RA	Lamb A., Roberts L.M., Lord J.M.;			
RT	"Nucleotide sequence of cloned cDNA coding for preproricin."			
RL	Eur. J. Biochem. 148:265-270(1985).			
RN	[4]			
RP	SEQUENCE OF 36-302.			
RA	Yoshitake S., Funatsu G., Funatsu M.;			
RT	"Isolation and sequences of peptic peptides, and the complete			
RT	sequence of ile chain of ricin-D."			
RL	Agric. Biol. Chem. 42:1267-1274(1978).			
RN	[5]			
RP	SEQUENCE OF 315-576.			
RA	Funatsu G., Kimura M., Funatsu M.;			
RT	"Primary structure of Ala chain of ricin D.;"			
RL	Agric. Biol. Chem. 43:2221-2224(1979).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.			
RX	MEDLINE=90344223; PubMed=1368517;			
RA	Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu G.;			
RT	"Structural analyses of sugar chains from ricin A-chain variant.;"			
RL	Agric. Biol. Chem. 54:157-162(1990).			
RN	[7]			
RP	REVIEW.			
RX	MEDLINE=21480122; PubMed=11595634;			
RA	Olsnes S., Kozlov J.V.;			

ALIGNMENTS

RT "Ricin."; CC
 RL Toxicon 39:1723-1728(2001). CC
 [8] CC
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). CC
 RX MEDLINE=87165983; PubMed=3558397; CC
 RA Monfort W., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B., CC
 Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.; CC
 RT "The three-dimensional structure of ricin at 2.8 Å."; CC
 J. Biol. Chem. 262:5398-5403(1987). CC
 [9] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=91352004; PubMed=1881881; CC
 RA Katzin B.J., Collins E.J., Robertus J.D.; CC
 RT "Structure of ricin A-chain at 2.5 Å."; CC
 RL Proteins 10:251-259(1991). CC
 [10] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. CC
 RX MEDLINE=91352005; PubMed=1881882; CC
 RA Rutenber E., Robertus J.D.; CC
 RT "Structure of ricin B-chain at 2.5-Å resolution."; CC
 RL Proteins 10:260-269(1991). CC
 [11] CC
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=95082010; PubMed=7990130; CC
 RA Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J., CC
 Paupit R.A.; CC
 RT "X-ray structure of recombinant ricin A-chain at 1.8-Å resolution."; CC
 RL J. Mol. Biol. 244:410-422(1994). CC
 [12] CC
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215. CC
 RX MEDLINE=96374222; PubMed=8780513; CC
 RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M., CC
 Molina-Svinth M.C., Robertus J.D.; CC
 RT "Structure and activity of an active site substitution of ricin A CC
 chain."; CC
 RL Biochemistry 35:11098-11103(1996). CC
 [13] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=97240820; PubMed=9086280; CC
 RA Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W., CC
 Robertus J.D.; CC
 RT "Structure-based identification of a ricin inhibitor."; CC
 RL J. Mol. Biol. 266:1043-1049(1997). CC
 [14] CC
 RP MUTAGENESIS. CC
 RX MEDLINE=93165632; PubMed=1287657; CC
 RA Kin Y., Robertus J.D.; CC
 RT "Analysis of several key active site residues of ricin A chain by CC
 mutagenesis and X-ray crystallography."; CC
 RL Protein Eng. 5:775-779(1992). CC
 CC
 CC -!- FUNCTION: Ricin is highly toxic to animal cells and to a less CC
 extent to plant cells. The A chain is responsible for inhibiting CC
 protein synthesis through the catalytic inactivation of 60S CC
 ribosomal subunits. It acts as a glycosidase that removes a CC
 specific adenine residue from an exposed loop of 28S ribosomal CC
 RNA. As this loop is involved in the binding of elongation CC
 factors, the modified ribosomes are unable to support protein CC
 synthesis. The A chain can inactivate a few thousand ribosomes CC
 per minute, thus inactivating them faster than the cell can make CC
 new ones. A single A-chain molecule can therefore kill an animal CC
 cell. The B chain binds to cell receptors and facilitates the CC
 entry into the cell of the A chain; B chains are also responsible CC
 for cell agglutination (lectin activity). It binds to beta-D- CC
 galactopyranoside moieties. CC
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one CC
 specific adenosine on the 28S rRNA. CC
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains. CC
 CC -!- DOMAIN: The B chain is composed of two domains, each domain CC
 consists of 3 homologous subdomains (alpha, beta, gamma). CC
 CC -!- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE CC
 MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271. CC
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME- CC
 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. CC

CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains. CC
 CC -!- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS CC
 WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3). CC
 CC -!- DATABASE: NAME=Protein Spotlight; CC
 CC NOTE=Issue 31 of February 2003; CC
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt031.html". CC
 CC
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 or send an email to license@isb-sib.ch). CC
 CC
 CC EMBL; X03179; CAA26939.1; - CC
 EMBL; X52908; CAA37095.1; - CC
 EMBL; X02388; CAA26230.1; - CC
 EMBL; A12892; CAA01058.1; - CC
 PIR; A24041; RUCSD. CC
 PDB; 2AAL; 31-JAN-94. CC
 PDB; 2AAL; 31-JAN-94. CC
 PDB; 1APG; 31-OCT-93. CC
 PDB; 1FMP; 31-OCT-93. CC
 PDB; 1IFS; 14-JAN-98. CC
 PDB; 1IFS; 14-JAN-98. CC
 PDB; 1IFT; 14-JAN-98. CC
 PDB; 1IFU; 14-JAN-98. CC
 PDB; 1LTC; 31-OCT-93. CC
 PDB; 1OBS; 16-JUN-97. CC
 PDB; 1OBT; 16-JUN-97. CC
 PDB; 1BR5; 02-SEP-98. CC
 PDB; 1BR6; 02-SEP-98. CC
 PDB; 1IL3; 16-JAN-02. CC
 PDB; 1IL4; 16-JAN-02. CC
 PDB; 1IL3; 16-JAN-02. CC
 GlycoSuiteDB; P02879; - CC
 InterPro; IPR000772; Ricin_B_lectin. CC
 InterPro; IPR001574; RIP. CC
 Pfam; PF00652; Ricin_B_lectin; 6. CC
 Pfam; PF00161; RIP; 1. CC
 PRINTS; PR00396; SHIGARICIN. CC
 SMART; SM00458; RICIN; 2. CC
 PROSITE; PS02031; RICIN B LECTIN; 2. CC
 PROSITE; PS00275; SHIGA_RICIN; 1. CC
 Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; CC
 KW Glycoprotein; Lectin; Signal; 3D-structure. CC
 FT SIGNAL 1 35 CC
 FT CHAIN 1 302 CC
 FT CHAIN 36 302 CC
 FT PEPTIDE 303 314 CC
 FT CHAIN 315 576 CC
 FT CHAIN 321 448 CC
 FT DOMAIN 451 575 CC
 FT DOMAIN 451 575 CC
 FT REPEAT 331 373 CC
 FT REPEAT 374 414 CC
 FT REPEAT 417 449 CC
 FT REPEAT 462 497 CC
 FT REPEAT 501 540 CC
 FT REPEAT 543 570 CC
 FT ACT SITE 212 212 CC
 FT ACT SITE 294 318 CC
 FT DISULFID 334 353 CC
 FT DISULFID 377 394 CC
 FT DISULFID 465 478 CC
 FT DISULFID 504 521 CC
 FT CARBOHYD 45 45 CC
 FT CARBOHYD 271 271 CC
 FT CARBOHYD 409 409 CC
 FT CARBOHYD 449 449 CC
 FT CONFLICT 76 76 CC
 FT CONFLICT 551 551 CC
 FT STRAND 43 47 CC
 FT TURN 49 50 CC
 N-LINKED (GLCNAC. . .) CC
 /FTID=CAR_000080. CC
 N-LINKED (GLCNAC. . .) (IN MINOR FORM). CC
 /FTID=CAR_000081. CC
 N-LINKED (GLCNAC. . .) CC
 N-LINKED (GLCNAC. . .) CC
 E -> D (IN REF. 3). CC
 A -> R (IN REF. 3). CC

Query Match 99.1%; Score 1010; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIVLPVLPNRVGLPINQRFILVEL 62
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIVLPVLPNRVGLPINQRFILVEL 97

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFAGN 122
 DB 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFAGN 157

QY 123 YDRLEQAGNLRNENELGNGLPBEAISALYYVYSTGTQTLPTLARSFIICMISEAAARFQ 182
 DB 158 YDRLEQAGNLRNENELGNGLPBEAISALYYVYSTGTQTLPTLARSFIICMISEAAARFQ 217

QY 183 YIEGEMTRIRYNRRS 198
 DB 218 YIEGEMTRIRYNRRS 233

RESULT 2
 AGGL RICCO STANDARD; PRT; 564 AA.
 AC P06750;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (xRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosidia I; Malpighiales; Euphorbiaceae; Ricinus.
 ON NCBI_TaxID=3988;
 RN [1]
 RP MEDLINE=86059449; PubMed=2999130;
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";
 RL J. Biol. Chem. 260:15682-15686(1985).
 RN [2]
 RP SEQUENCE OF 303-564.
 RC TISSUE=Seed;
 RA Araki T., Yoshioka Y., Funatsu G.;
 RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";
 RL Biochim. Biophys. Acta 872:277-285(1986).
 RN [3]
 RP SEQUENCE OF 303-337.
 RX MEDLINE=80178723; PubMed=6768555;
 RA Lin T.-S., Li S.-L.;
 RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
 RL Eur. J. Biochem. 105:453-459(1980).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC EMBL; M12089; AAA33869.1; -
 DR EMBL; S40368; AAB22584.1; -

DR PIR; A24261; RLCSAG.
 DR HSSP; P02879; 1BR6.
 DR GlycoSuiteDB; P06750; -
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; P003396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Plant defense: Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; lectin; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 AGGLUTININ A CHAIN.
 FT PROPEP 291 302 LINKER PEPTIDE.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 405 437 1-GAMMA.
 FT REPEAT 489 528 2-ALPHA.
 FT REPEAT 531 558 2-BETA.
 FT ACT_SITE 200 200 2-GAMMA.
 FT DISULFID 282 306 BY SIMILARITY.
 FT DISULFID 322 341 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 337 397 N-LINKED (GLCNAC. .).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. .).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 362 362 N -> D (IN REF. 2).
 FT CONFLICT 374 374 R -> G (IN REF. 2).
 FT CONFLICT 404 404 R -> T (IN REF. 2).
 FT CONFLICT 552 552 F -> V (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;
 Query Match 90.3%; Score 920.5; DB 1; Length 564;
 Best Local Similarity 91.8%; Pred. No. 3.5e-78;
 Matches 180; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIVLPVLPNRVGLPINQRFILVEL 62
 DB 27 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIVLPVLPNRVGLPINQRFILVEL 86

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFAGN 122
 DB 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNSFTAFAGN 146

QY 123 YDRLEQAGNLRNENELGNGLPBEAISALYYVYSTGTQTLPTLARSFIICMISEAAARFQ 182
 DB 147 YDRLEQAGNLRNENELGNGLPBEAISALYYVYSTGTQTLPTLARSFMVCIOMISEAAARFQ 205

QY 183 YIEGEMTRIRYNRRS 198
 DB 206 YIEGEMTRIRYNRRS 221

RESULT 3
 ABRC ABRPR
 ID ABRC ABRPR STANDARD; PRT; 562 AA.
 AC P28550;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abrin-c precursor [Contains: Abrin-c A chain (xRNA N-glycosidase) (EC 3.2.2.22); Abrin-c B chain].
 DE Abrus precatorius (Indian licorice) (Crab's eye).
 OS

Best Local Similarity 45.5%; Pred. No. 2.4e-25;
Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

QY 5 QYPIINFNTAGATVQSYTNFIRAVRGLRTGADVRRHEIPVLPNRRVGLPINQRFTILVELSN 64
DB 35 QDOVIKFTTEGATSQSKQFIEALRQLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 92
QY 65 HAEISVTLALDVTNAVVGVRAGNSAYFFHPDPNQEDAEALTHLFTDVQNRYYTFAFGNYD 124
DB 93 SERESIEVGIDVTNAVVRAGSQQYFL---RDAPASASTYILFPGTQ-RYSLEFDSYG 148
QY 125 RLEQLAGNLRNRELTGNGLPEEASIALYVYSTGTQTLPTLARSFIIICIMISEARFOYI 184
DB 149 DIERWAHQTRFELSISGLQALTHAIS---FLRSGASNDDEAKRLIVLIQWASEARVRYI 205
QY 185 EGEHMRTRIR 193
DB 206 SNRVGVGSIIR 214

RESULT 4

ID	ABRR	ABRRP	STANDARD;	PRT;	527 AA.
AC	Q06077;	P81374;			
DT	15-DEC-1998	(Rel. 37, Created)			
DT	15-DEC-1998	(Rel. 37, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)				
DE	(EC 3.2.2.2); Abrin-b B chain).				
OS	Abrus precatorius (Indian licorice) (Crab's eye).				
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.				
OX	NCBI_TaxID=3816;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93132738; PubMed=8421313;				
RC	Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;				
RT	"Primary structure of three distinct isoabrin subunits determined by cDNA				
RT	sequencing. Conservation and significance.";				
RL	J. Mol. Biol. 229:263-267(1993).				
RP	[2]				
RP	SEQUENCE OF 260-527.				
RP	TISSUE=Seed;				
RC	MEDLINE=931169023; PubMed=7763422;				
RC	Kimura M., Sumizawa T., Funatsu G.;				
RT	"The complete amino acid sequences of the B-chains of abrin-a and				
RT	abrin-b toxic proteins from the seeds of Abrus precatorius.";				
RL	Bioess. Biotechnol. Biochem. 57:166-169(1993).				
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN				
CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL				
CC	SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.				
CC	ABRIN-A IS MORE TOXIC THAN RICIN.				
CC	-1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT				
CC	FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT				
CC	PRECEDES ENDOCYTOSIS.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.				
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN				
CC	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).				
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-				
CC	INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.				
CC	-1- SIMILARITY: Contains 2 ricin B-type lectin domains.				

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DR EMBL, M58345; AAA32625.1; -.
DR FIR, S32430; S32430.
DR HSP, P11140; IABR.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PR00652; Ricin_B_lectin; 6.
DR Pfam; PR00161; RIP_1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
FT CHAIN 1 250 ABRIN-B A CHAIN.
FT PEPTIDE 251 260 LINKER PEPTIDE.
FT CHAIN 261 527 ABRIN-B B CHAIN.
FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.
FT DOMAIN 402 526 RICIN B-TYPE LECTIN 2.
FT REPEAT 282 324 1-ALPHA.
FT REPEAT 325 365 1-BETA.
FT REPEAT 368 400 1-GAMMA.
FT REPEAT 413 448 2-ALPHA.
FT REPEAT 452 491 2-BETA.
FT REPEAT 494 527 2-GAMMA.
FT ACT_SITE 163 163 BY SIMILARITY.
FT DISULFID 246 268 INTERCHAIN (BY SIMILARITY).
FT DISULFID 285 304 BY SIMILARITY.
FT DISULFID 328 345 BY SIMILARITY.
FT DISULFID 416 429 BY SIMILARITY.
FT DISULFID 455 472 BY SIMILARITY.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 282 282 N -> D (IN REF. 2).
FT CONFLICT 291 291 D -> N (IN REF. 2).
FT CONFLICT 350 351 AE -> PQ (IN REF. 2).
FT CONFLICT 378 378 S -> N (IN REF. 2).
FT CONFLICT 426 426 L -> M (IN REF. 2).
FT CONFLICT 428 428 Y -> D (IN REF. 2).
FT CONFLICT 431 431 N -> S (IN REF. 2).
FT CONFLICT 484 484 R -> K (IN REF. 2).
FT CONFLICT 491 491 N -> S (IN REF. 2).
FT CONFLICT 493 493 H -> Y (IN REF. 2).
FT CONFLICT 502 502 R -> G (IN REF. 2).
FT CONFLICT 509 509 E -> Q (IN REF. 2).
FT CONFLICT 513 513 H -> W (IN REF. 2).
FT CONFLICT 516 516 H -> T (IN REF. 2).
SQ SEQUENCE 527 AA; 59114 MM; 3253AB490CE9494A CRC64;
Query Match 33.9%; Score 345; DB 1; Length 527;
Best Local Similarity 45.5%; Pred. No. 1.4e-24;
Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;
QY 5 OYPIINFTTAGATVQSYTHFIRAVRGRLTGADVREHPIVLPNVRGVLPIQNRILVELSN 64
Db 1 QDVQIKFTTGATGQSYKQFIEALRDLTGG--LIHGIPVLPDPTTLQERNRIVVELSN 58
QY 65 HAEISVTLADVTNAYVYVGRAGNSAYFFHPDQEDAEALTHLFDVQVRYTFAGGNYD 124
Db 59 SDTESIEAGIDVSNAYVAVRAGNSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
QY 125 RLQOLAGNRENTLGNPLIEEISALYYSTGTQTLPLARSLFICIMISAARFQYI 184
Db 115 DLRLARQTRQQIPLGLQALRHAISEL----QSGTDDQEIARTLIVIQMASEAARYRFI 170
QY 185 EGENRTIRYN 195
Db 171 SYRVGVSIKRN 181
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RESULT 5

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RIPT_TRIKI
ID RIPT TRIKI STANDARD; PRT; 289 AA.
AC P09989;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein alpha-trichosanthin precursor
DE (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz;
RX MEDLINE=91153657; PubMed=1999291;
RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
RT "Cloning of trichosanthin cDNA and its expression in Escherichia
coll.>";
RL Gene 97:267-272(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz; TISSUE=Leaf;
RX MEDLINE=90256790; PubMed=2341400;
RA Chow T., Feldman R.A., Lovett M., Piatak M.;
RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
type I ribosome-inactivating protein.";
RL J. Biol. Chem. 265:8670-8674(1990).
RN [3]
RP SEQUENCE OF 24-270.
RC STRAIN=Maximowicz; TISSUE=Tuberous root;
RX MEDLINE=90256789; PubMed=2341399;
RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
Wu P., Hwang K., Piatak M.;
RT "Primary amino acid sequence of alpha-trichosanthin and molecular
models for abrin A-chain and alpha-trichosanthin.";
RL J. Biol. Chem. 265:8665-8669(1990).
RN [4]
RP SEQUENCE OF 24-270.
RC TISSUE=Tuberous root;
RX Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
application.";
RL Pure Appl. Chem. 58:789-798(1986).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RX MEDLINE=94344957; PubMed=8056085;
RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
RT "Structure of trichosanthin at 1.88-A resolution.";
RL Proteins 19:4-13(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=95344383; PubMed=7619070;
RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
RT "Studies on crystal structures, active-centre geometry and
depurinating mechanism of two ribosome-inactivating proteins.";
RL Biochem. J. 309:285-298(1995).
CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
FT ACT_SITE 183 BY SIMILARITY.
FT CARBOHYD 25 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;

Query Match 33.5%; Score 341.5; DB 1; Length 282;
Best Local Similarity 48.0%; Pred. NO. 1.9e-24;
Matches 86; Conservative 23; Mismatches 57; Indels 13; Gaps 7;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPN-RVGLPINQRFILVELSNHAE 67
DB 24 INFSLIGATGATKTKTIRNLTKLTGTPRVYDIPVLRNAAAGL---ARFQVTLNYNG 80
QY 69 LSVTLALDVNAVVGVRAGNSAYFFHPDQDEAETHLFTDVQVRYTFAGGNYDRLE 127
DB 81 ESVTVALDVNAVVGVRAGNSAYFFHPDQDEAETHLFTDVQVRYTFAGGNYDRLE 127
QY 128 QLAGNL-RENIELGNGPLREASALVYVSTGGTQPLTARSFTICQMISEARFOYIE 185
DB 137 TAGGRISRENIELGNGPLREASALVYVSTGGTQPLTARSFTICQMISEARFOYIE 191

RESULT 7
RIPS TRIKI
ID RIPS TRIKI STANDARD; PRT; 289 AA.
AC P24478;
DT 01-MAR-1992 (Rel. 21, Created)
DE 15-DEC-1998 (Rel. 37, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein karasurin precursor (rRNA
DE N-glycosidase) (EC 3.2.2.22).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root tuber;
RX MEDLINE=92005921; PubMed=1914000;
RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogiwara Y.;
RT "The complete amino acid sequence of an abortifacient protein,
RT karasurin."
RL Chem. Pharm. Bull. 39:1244-1249 (1991).
CC -1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
CC 60S RIBOSOMAL SUBUNITS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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CC EMBL; AB000666; BAA21786.1; -.
DR PIR; JC5606; JC5606.
DR PIR; JUC393; JUC393.
DR HSSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 270 KARASURIN-C.
FT CHAIN 24 270 KARASURIN-A.
FT PROPEP 271 289 REMOVED IN MATURE FORM.
FT ACT_SITE 183 BY SIMILARITY.
SQ SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;

Query Match 33.2%; Score 338; DB 1; Length 289;
Best Local Similarity 40.0%; Pred. NO. 2.9e-24;
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRGLPINQRFILVELSNHAE 68
DB 25 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALHLTNVADE 81
QY 69 SVTLALDVNAVVGVRAGNSAYFFHPDQDEA-EAETHLFTDVQVRYTFAGGNYDRLE 127
DB 82 TISVAIDVTNVVVGVRAGDTSYFF---NEASATEAAKYVFKDAKRVLTSPYSGNYERLQ 138
QY 128 QLAGNLRENIELGNGPLREASALVYVSTGGTQPLTARSFTICQMISEARFOYIE 187
DB 139 IAAGKIRENIPLGLPALDSAITLTFYNNAN-----SAASALMWLIQSTSEARFYKIEQ 193
QY 188 METRI 192
DB 194 IGRKV 198

RESULT 8
NIGB SAMNI
ID NIGB SAMNI STANDARD; PRT; 563 AA.
AC P33183; P33184; P93542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
DE (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bark;
RX MEDLINE=96215449; PubMed=8647092;
RA Van Damme E.-J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
RT (nigrin b), a GalNAC-specific type-2 ribosome-inactivating protein
RT from the bark of elderberry (Sambucus nigra).";
RL Eur. J. Biochem. 237:505-513 (1996).
RN [2]
RP SEQUENCE OF 26-49 AND 298-321.
RC TISSUE=Bark;
RX MEDLINE=94003077; PubMed=8400135;
RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
RT "Isolation and partial characterization of nigrin b, a non-toxic
RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
RT nigra L.";
RL Plant Mol. Biol. 22:1181-1186 (1993).
CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
```


Db 63 SIEGVIDTWAYVAYRAGTQSPFLRDPASSAD-----YLFCT-DQHSLEPFYGVGDL 116
Qy 127 EQLAGNLRNIELNGPLEEAISSALYYSTGGTQPLTFLARSFICIMISEAARFOYIEG 186
Db 117 ERWAHQSRQIFLGLQALTHGIS---FFRSQGNNEEKANTLIVIQWVAEAFRIYSN 173
Qy 187 EMRTIR 193
Db 174 RVRVSIQ 180

RESULT 10

RIP1_BRYDI
AC P33185; Q9S819; STANDARD; PRT; 290 AA.
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(EC 3.2.2.22) (BDL).
OS Bryonia dioica (Red bryony).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC Eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_TaxID=3652;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC TISSUE=Leaf;
RX MEDLINE=97228081; PubMed=9115985;
RA Gwialak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
RA Siegall C.B.;
RT "Molecular, biological, and preliminary structural analysis of
recombinant bryodin I, a ribosome-inactivating protein from the plant
Bryonia dioica.";
RL Biochemistry 36:3095-3103 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Siegall C.B.;
RT "Cloning and expression of a gene encoding bryodin I from Bryonia
dioica.";
RL Patent number US5541110, 30-JUL-1996.
RN [3]
RP SEQUENCE OF 24-66.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
RA Lappi D.;
RT "N-terminal sequence of some ribosome-inactivating proteins.";
RL Int. J. Pept. Protein Res. 33:263-267 (1989).
RN [4]
RP SEQUENCE OF 24-43.
RC TISSUE=Root;
RX MEDLINE=95151812; PubMed=7849072;
RA Siegall C.B., Gwialak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marguardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
Bryonia dioica and their utility as carcinoma-reactive
immunoconjugates.";
RL Bioconj. Chem. 5:423-429 (1994).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO
PRODUCE A SHORTER PROTEIN.
CC -!- BIOTECHNOLOGY: Especially useful as immunotoxin for
pharmacological applications as it has low toxicity in rats and
mice but is potent once inside target cells.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; I24020; --; NOT_ANNOTATED_CDS.
DR PIR; S16491; S16491.
DR PDB; 1BRY; 04-MAR-98.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW 3D-structure; Multigene family; Glycoprotein; Signal.
CC -----
FT SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
FT CHAIN 24 270 MISSING IN MATURE PROTEIN.
FT PROPEP 271 290 BY SIMILARITY.
FT ACT_SITE 183 183
FT ACT_SITE 212 212
FT CARBOHYD 214 214
FT CARBOHYD 250 250
FT MUTAGEN 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 61 65 E->K: REDUCES ACTIVITY 10-FOLD.
FT STRAND 25 28 RSSIS -> LRHXI (IN REF. 3).
FT TURN 30 31
FT HELIX 34 46
FT TURN 47 47
FT STRAND 50 54
FT TURN 55 56
FT STRAND 57 60
FT HELIX 66 69
FT STRAND 70 76
FT TURN 82 88
FT TURN 89 92
FT STRAND 93 99
FT TURN 100 101
FT STRAND 102 105
FT HELIX 109 114
FT TURN 115 117
FT TURN 120 121
FT STRAND 124 127
FT HELIX 134 141
FT TURN 142 142
FT STRAND 145 147
FT HELIX 150 150
FT TURN 152 163
FT TURN 164 165
FT HELIX 167 186
FT STRAND 187 187
FT HELIX 188 196
FT STRAND 202 202
FT HELIX 206 213
FT TURN 214 214
FT HELIX 215 225
FT TURN 226 230
FT STRAND 231 239
FT TURN 241 242
FT STRAND 245 250
FT TURN 251 252
FT HELIX 254 257
FT TURN 258 259
FT STRAND 260 260
FT STRAND 263 263
FT HELIX 266 268
SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;

Query Match 30.6%; Score 312; DB 1; Length 290;
Best Local Similarity 37.3%; Pred. No. 7.7e-22;
Matches 69; Conservative 46; Mismatches 58; Indels 12; Gaps 5;


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QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINQRFILVELSNHAEL 68
Db 25 VSRFUGATTSSYGVIKNLREALPYERKV-YNIPLL--RSSISGSGRYTLHLHNTNAYADE 81

QY 69 SVTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
Db 82 TISVAVDVNTVIMGYLAGDVSYFF--NEASATEAAKFVKDAKKVTLPLPSGNYERLQ 138

QY 128 QLGNLRENIELGNGLPEEAISALYYSTGTQTLFLARSFIIQMISEARFOYIEGE 187
Db 139 TAAGKIRENIPGLPALDSAITLLYYTAS-----SAASALLVLIQSTAESARYKFIHQ 193

QY 188 MRTRI 192
Db 194 IGRV 198

RESULT 11
RIPB LUFYC STANDARD; PRT; 250 AA.
AC P22851;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=91248488; PubMed=1368666;
RA Islam M.R., Hirayama H., Funatsu G.;
RT "Complete amino acid sequence of luffin-B, a ribosome-inactivating
RT protein from sponge gourd (Luffa cylindrica) seeds.";
RL Agric. Biol. Chem. 55:229-238(1991).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR PIR; JN0108; JN0108.
DR HSSP; P16094; 1AHC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin.
FT ACT_SITE 160 160 BY SIMILARITY.
FT SEQUENCE 250 AA; 27293 MW; F01A8DC8A1078700 CRC64;
Query Match 29.5%; Score 300.5; DB 1; Length 250;
Best Local Similarity 34.2%; Pred. No. 7.6e-21;
Matches 64; Conservative 48; Mismatches 64; Indels 11; Gaps 3;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINQRFILVELSNHAEL 68
Db 3 VSGFSGADSKGYSKFTALRKALPSKEKVNIPILLPSASGA---SRVILMQLSNYDAK 59

QY 69 SVTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQ 128
Db 60 AITMAIDVNTVIMGYLVNVTSYF---ANESDAKLASQVFKGSTLVTLPYSGNVERLQN 116

QY 129 LAGNLRENIELGNGLPEEAISALYYSTGTQTLFLARSFIIQMISEARFOYIEGEM 188
Db 117 AAGKIREKIPGLPALDSALTSTFIHYDS-----TAAAFVLIQTAAEFKIEGOI 171

QY 189 RTRIRYN 195
Db 172 IERIPKN 178

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RESULT 12
RIP1 CUCFI STANDARD; PRT; 286 AA.
ID RI1 CUCFI
AC Q9FRX4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Cucumis figareii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=131071;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada T., Ohki S.T., Osaki T.;
RT "Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareii.";
RL Plant Biotechnol. 17:337-340(2000).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB045560; BAB19677.1; -.
CC HSSP; P16094; 1AHC.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
FT ACT_SITE 185 185 BY SIMILARITY.
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 286 AA; 31771 MW; 4EFD4965604DA41 CRC64;
Query Match 29.1%; Score 296.5; DB 1; Length 286;
Best Local Similarity 34.4%; Pred. No. 2.1e-20;
Matches 65; Conservative 47; Mismatches 64; Indels 13; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINQRFILVELSNHAEL 67
Db 28 VKFSLGNNHKSYSKFTISMNALPNAGDI-YNIPLLVPSISG---SRVILMQLSNYEG 83

QY 68 LSVTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
Db 84 NITMAVDVNTVIMGYLVNVTSYF---NETDAQLASKFVFGTKSTLPLPSGNYQKLIQ 140

QY 128 QLGNLRENIELGNGLPEEAISALYYSTGTQTLFLARSFIIQMISEARFOYIEGE 187
Db 141 SVARKERDSIPLGFALDSALTSTLYYDSRAPI-----AFLVLIQTAAEFKIEKQ 195

QY 188 MRTRIRYN 196
Db 196 IIRISVSK 204

RESULT 13

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MLA_VISAL ID_MLA_VISAL STANDARD; PRT; 254 AA.

AC P81446;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosidase) (EC 3.2.2.22).
 DE Viscum album (European mistletoe).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Santalaceae; Viscum.
 NCBI_TaxID=3972;
 [1]
 RN SEQUENCE.
 RP STRAIN=Subsp. album;
 RC MEDLINE=97134581; PubMed=8980141;
 RA Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
 RA Voelter W.;
 RL "Complete amino acid sequence of the A chain of mistletoe lectin I."; FEBS Lett. 399:153-157(1996).
 CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN. B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -!- PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.
 CC -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 2 RIP SUBFAMILY.
 DR PIR; PD0018; PD0018.
 DR HSSP; P11140; IABR.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.
 KW Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.
 FT CATH SITE 165 165
 FT CATH SITE 112 112
 FT CATH SITE 15 15
 FT CATH SITE 66 66
 FT CATH SITE 112 112
 FT CATH SITE 116 116
 FT CATH SITE 133 133
 FT CATH SITE 140 140
 FT CATH SITE 144 144
 FT CATH SITE 151 151
 FT CATH SITE 179 179
 FT CATH SITE 184 184
 FT CATH SITE 190 190
 FT CATH SITE 218 218
 FT CATH SITE 223 223
 FT CATH SITE 231 231
 FT CATH SITE 235 235
 SQ SEQUENCE 254 AA; 28478 MW; 53BAF98D3E0FFE67 CRC64;
 Query Match 28.1%; Score 286; DB 1; Length 254;
 Best Local Similarity 38.4%; Pred. No. 1.7e-19;
 Matches 81; Conservative 36; Mismatches 56; Indels 38; Gaps 10;
 QY 13 TAGATGQSYNTFRAVGRLLTGADVRHEIPVLPNVRGLPIN--QRFLVELSNHAELSV 70
 DB 9 THQTTGEFRTILRDYVSSGS-PSNEIFLL-RQSIPVSDAQRFLVELTNGQDSV 66
 QY 71 TLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQLA 130

Db 67 TAAIDVTNAYVAYAGDQSYFLR-DAPRGAE--THLTGT-TRSLPFGNSYDPERVA 122
 QY 131 GNLRNIEIENGPLEEALISALYYSTGGTQLPFTLARSFCIOMISEAARF-----Q 182
 Db 123 GH-RDQIPLGIDLIQSVTALRF---PGGSTRQARSILLIOMISEAARFNFILWRYRQ 178
 QY 183 YIE-----GEMRTRIRYN 195
 Db 179 YINGSGASFDPVYMLELTSWGQOSTQVQHS 209
 RESULT 14
 ID_RIPA_LUCFY STANDARD; PRT; 277 AA.
 AC Q00465;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.22).
 OS Luffia cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
 NCBI_TaxID=3670;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Seed;
 RC MEDLINE=92288316; PubMed=1600156;
 RA Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
 RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffia cylindrica."; Plant Mol. Biol. 18:1199-1202(1992).
 RL Plant Mol. Biol. 18:1199-1202(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
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 CC EMBL; X62371; CAA44229.1; --
 CC PIR; S22494; S22494.
 CC HSSP; P16094; IABC.
 CC InterPro; IPR001574; RIP.
 CC Pfam; PF00161; RIP; 1.
 CC PRINTS; PR00396; SHIGARICIN.
 CC PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 FT SIGNAL 1 19
 FT CHAIN 20 277 RIBOSOME-INACTIVATING PROTEIN LUFFIN-ALPHA.
 FT ACT_SITE 179 179 BY SIMILARITY.
 FT SEQUENCE 277 AA; 30212 MW; EAL7FC27998C25AC CRC64;
 SQ SEQUENCE 27.9%; Score 284.5; DB 1; Length 277;
 Best Local Similarity 33.5%; Pred. No. 2.7e-19;
 Matches 63; Conservative 45; Mismatches 69; Indels 11; Gaps 3;
 QY 9 INFATTAGATVQSYNTFRAVGRLLTGADVRHEIPVLPNVRGLPINORFILVELSNHAEL 68
 Db 22 VRFSLGSSTSYSKFICDLRLKLPNGTVYNTPLLSASGA---SRYTLMTLSNDGX 78
 QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 128
 Db 79 AITVADVNTVNYIMGVNSTSYFF---NESDAKLASQYVFKGSTIVTLPSYGNIEKLQT 135

QY 129 LAGNLENELNGPLEEALISALYYSTGGTOLPTLARSFFIICQWISAEARFQYIEGEM 188
Db 136 AAGKIREKIPLEGFPALDSAITLLEHYDS-----TAAAFILVLIQTAAERFKYIEGQI 190
QY 189 RTRIRYNR 196
Db 191 IERISKQ 198

RESULT 15
RIP2 MOMBA STANDARD; PRT; 286 AA.
AC P29339;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein momordin II precursor (rRNA
DE N-glycosidase) (EC 3.2.2.22).
OS Momordica balsamina (Bitter melon)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3672;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=93027170; PubMed=1408771;
RT Ortigao M., Better M.;
RT "Momordin II, a ribosome inactivating protein from Momordica
RT balsamina, is homologous to other plant proteins.";
RT Nucleic Acids Res. 20:4662-4662(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.

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EMBL; Z12175; CAA78166.1; -.
DR F1R; S25560; S25560.
DR FDB; 1CF5; 07-JUN-99.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
FT II.
FT ACT_SITE 181 181 BY SIMILARITY
FT SEQUENCE 286 AA; 32031 MW; 3B89FFAE6B25986 CRC64;
Query Match 27.6%; Score 281; DB 1; Length 286;
Best Local Similarity 35.1%; Pred. No. 5.9e-19;
Matches 68; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

QY 2 VPKQPIINFTTAGATVQSYTNFIRAVRGLTGTADVRHEIPVLPNVRGLPINQRPILVE 61
Db 18 VPTAKGVNFDLSTAKTYTKTFIEDFRATLPFSHKV-YDIPLLXSTIS--DSRRFILLD 74
QY 62 LSNHAEISVTLADVTNAVGVGNAGSAYVEFPDQEDAEATHLFTDVQNYTFACGG 121
Db 75 LTIAYETISVADVTNAVVRTRDVSFF--KESPEAYNILFKGTR-KITLPYTG 130
QY 122 NYDRLEQLAGNLENELNGPLEEALISALYYSTGGTOLPTLARSFFIICQWISAEARF 181

Db 131 NYENLQTAHAKIRENIDLGLEPALSSAITLIFYNA-----QSAPSAIIVLIQTAAERF 185
QY 182 QYIEGEMFTRIRYN 195
Db 186 KYIERHVAKYVATN 199
Search completed: February 10, 2004, 16:23:24
Job time : 6.60489 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 26.4196 Seconds
(without alignments)
1933.961 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019
Sequence: 1 MVPKQYPIINTAGATVQS.....ARFQVIEGEMTRINYNRS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	98.8	541	10 Q41174	Q41174 ricinus com
2	401.5	39.4	580	10 Q94BW3	Q94BW3 cinnamomum
3	397.5	39.0	580	10 Q94BW4	Q94BW4 cinnamomum
4	397.5	39.0	581	10 Q94BW5	Q94BW5 cinnamomum
5	395.5	38.8	549	10 Q9FV22	Q9FV22 cinnamomum
6	350.5	34.4	563	10 Q04367	Q04367 sambucus ni
7	347.5	34.1	564	10 Q9AVR2	Q9AVR2 sambucus eb
8	344.5	33.8	528	10 Q06076	Q06076 abrus preca
9	340	33.4	289	10 Q94KE4	Q94KE4 trichosan
10	338	33.2	247	10 Q9LRE3	Q9LRE3 trichosan
11	338	33.2	289	10 Q41216	Q41216 trichosan
12	336.5	33.0	252	10 Q38760	Q38760 abrus preca
13	330.5	32.4	563	10 Q945S2	Q945S2 sambucus ni
14	330.5	32.4	563	10 Q8GT32	Q8GT32 sambucus ni
15	329.5	32.3	252	10 Q38761	Q38761 abrus preca
16	324	31.8	270	10 Q8LPV7	Q8LPV7 trichosan

17	323.5	31.7	251	10 Q96236	Q96236 abrus preca
18	322.5	31.6	251	10 Q96237	Q96237 abrus preca
19	319	31.3	565	10 Q04071	Q04071 sambucus ni
20	317	31.1	270	10 Q41611	Q41611 trichosan
21	316.5	31.1	251	10 Q96235	Q96235 abrus preca
22	314.5	30.9	547	10 Q9M6E9	Q9M6E9 abrus preca
23	310.5	30.5	566	10 Q04072	Q04072 sambucus ni
24	307.5	30.2	278	10 Q00980	Q00980 luffa cylin
25	291	28.6	570	10 Q41358	Q41358 sambucus ni
26	285	28.0	249	10 Q8LKQ5	Q8LKQ5 viscum albu
27	285	28.0	570	10 Q22415	Q22415 sambucus ni
28	283.5	27.8	604	10 Q9M654	Q9M654 polygonatum
29	283	27.8	251	10 Q8LKQ4	Q8LKQ4 viscum albu
30	282	27.7	254	10 Q8LKQ6	Q8LKQ6 viscum albu
31	280	27.5	264	10 Q9FSH2	Q9FSH2 momordica c
32	279	27.4	286	10 Q9FUV7	Q9FUV7 momordica c
33	278	27.3	293	10 Q8S452	Q8S452 jatrophia cu
34	277.5	27.2	565	10 Q8W243	Q8W243 viscum albu
35	277	27.2	569	10 P93543	P93543 sambucus ni
36	275	27.0	531	10 Q8RXH6	Q8RXH6 viscum albu
37	274	26.9	286	10 Q41257	Q41257 momordica c
38	273	26.8	249	10 Q8RXH7	Q8RXH7 viscum albu
39	272	26.7	298	10 Q04358	Q04358 iris hollan
40	270	26.5	592	10 Q8W2E7	Q8W2E7 iris hollan
41	268	26.3	300	10 Q04356	Q04356 iris hollan
42	265.5	26.2	603	10 Q9M653	Q9M653 polygonatum
43	262.5	25.8	299	10 Q8GZN9	Q8GZN9 euphorbia s
44	261	25.6	293	10 Q8VYU0	Q8VYU0 jatrophia cu
45	259	25.4	573	10 Q8W2E8	Q8W2E8 iris hollan

ALIGNMENTS

RESULT 1

Q41174
ID Q41174 PRELIMINARY; PRT; 541 AA.
AC Q41174;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92338377; PubMed=1633311;
RA Roberts L.M., Tregear J.W., Lord J.M.;
RT "Molecular cloning of ricin.;"
RL Targeted diagn. Ther. 7:81-97(1992).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; S40366; A822382.1; -.
DR HSSP; P02879; 1BR6.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hydrolase; Toxin.
FT NON TER 1
SQ SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;

Query Match 98.8%; Score 1007; DB 10; Length 541;
Best Local Similarity 99.5%; Pred. No. 1.7e-86;
Matches 195; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKOYPIINFTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62
DB 3 PKOYPIINFTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 122
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 122

QY 123 YDLEOLAGNLRNIELGNGLPEEASALYYSTGGTQPLTLARSFICQMISEAARFQ 182
DB 123 YDLEOLAGNLRNIELGNGLPEEASALYYSTGGTQPLTLARSFICQMISEAARFQ 182

QY 183 YIEGEMTRIRYNRS 198
DB 183 YIEGEMTRIRYNRS 198

RESULT 2
Q94BW3 ID Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY039803; AAK82450.1;
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; Ricin; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7F558 CRC64;

Query Match 39.4%; Score 401.5; DB 10; Length 580;
Best Local Similarity 50.0%; Pred. No. 2.8e-29;
Matches 94; Conservative 28; Mismatches 59; Indels 7; Gaps 5;

QY 6 YPIINFTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVWRDGSSTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 124
DB 92 AADSPVTLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 148

QY 125 RLEOLAGNLRNIELGNGLPEEASALYYSTGGTQPLTLARSFICQMISEAARFQ 184
DB 149 DLERVAGERREIEILGMDPLENALSINL--NQQRALARSLLIVVIQMAEAVRFRFI 206

Query Match 39.0%; Score 397.5; DB 10; Length 580;
Best Local Similarity 49.5%; Pred. No. 6.7e-29;
Matches 93; Conservative 30; Mismatches 58; Indels 7; Gaps 5;

QY 6 YPIINFTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVWRDGSSTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 124
DB 92 AADSPVTLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 148

QY 125 RLEOLAGNLRNIELGNGLPEEASALYYSTGGTQPLTLARSFICQMISEAARFQ 184
DB 149 DLERVAGERREIEILGMDPLENALSINL--NQQRALARSLLIVVIQMAEAVRFRFI 206

Query Match 39.0%; Score 397.5; DB 10; Length 580;
Best Local Similarity 49.5%; Pred. No. 6.7e-29;
Matches 93; Conservative 30; Mismatches 58; Indels 7; Gaps 5;

QY 6 YPIINFTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVWRDGSSTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 124
DB 92 AADSPVTLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGN 148

QY 125 RLEOLAGNLRNIELGNGLPEEASALYYSTGGTQPLTLARSFICQMISEAARFQ 184
DB 149 DLERVAGERREIEILGMDPLENALSINL--NQQRALARSLLIVVIQMAEAVRFRFI 206

OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039801; AAK82458.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR PRINTS; PR00161; RIP; 1.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS00396; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 581
FT POTENTIAL.
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN I.
SQ SEQUENCE 581 AA; 64215 MW; 658F5F8FBA3D196 CRC64;

Query Match 39.0%; Score 397.5; DB 10; Length 581;
Best Local Similarity 50.0%; Pred. No. 6.7e-29;
Matches 94; Conservative 27; Mismatches 60; Indels 7; Gaps 5;

QY 6 YPIINFTTAGATVQSYTFIRAVRGRLTGTADVRHEIPVLNVRGLPINQRFILVLSN- 64
DB 33 YQTVTFTTKATKTSYQFIEALRAQLASGEE-PHGIPVWRERSTVPDSKRFILVLSNW 91
QY 65 HAEISVTLALDVTNAYVYGVYAGNSAYFFHFDNODAEAIHTLFTDQNRVTEAFGGNYD 124
DB 92 AADSPVTLAVDTNAYVYVYRGSGSFLEENPD--PAIENLLPDTK-RYTFPFGSGYT 148
QY 125 RLEQLAGMLRENIENGNGLEAEISALYYVYGTGTQPLTLARSFICICMISEARFOYI 184
DB 149 DLEGVAGERREIEILLGMDPLENAISALWISNL--NQQRALARSLLVVIQWVAEVRFRFI 206
QY 185 EGEWRTI 192
DB 207 EYRVGSI 214

RESULT 5
Q9FV22
ID Q9FV22 PRELIMINARY; PRT; 549 AA.
AC Q9FV22
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
DE N-glycosidase) (fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RT "Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AF259548; AAF68978.2; -.
DR HSSP; P02879; 2AAL.

DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS00396; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Toxin.
FT NON_TER 1
FT CHAIN 1
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607CA44B0 CRC64;

Query Match 38.8%; Score 395.5; DB 10; Length 549;
Best Local Similarity 50.0%; Pred. No. 9.6e-29;
Matches 94; Conservative 27; Mismatches 60; Indels 7; Gaps 5;

QY 6 YPIINFTTAGATVQSYTFIRAVRGRLTGTADVRHEIPVLNVRGLPINQRFILVLSN- 64
DB 1 YQTVTFTTKATKTSYQFIEALRAQLASGEE-PHGIPVWRERSTVPDSKRFILVLSNW 59
QY 65 HAEISVTLALDVTNAYVYGVYAGNSAYFFHFDNODAEAIHTLFTDQNRVTEAFGGNYD 124
DB 60 AADSPVTLAVDTNAYVYVYRGSGSFLEENPD--PAIENLLPDTK-RYTFPFGSGYT 116
QY 125 RLEQLAGMLRENIENGNGLEAEISALYYVYGTGTQPLTLARSFICICMISEARFOYI 184
DB 117 DLEGVAGERREIEILLGMDPLENAISALWISNL--NQQRALARSLLVVIQWVAEVRFRFI 174
QY 185 EGEWRTI 192
DB 175 EYRVGSI 182

RESULT 6
Q04367
ID Q04367 PRELIMINARY; PRT; 563 AA.
AC Q04367
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
DE N-glycosidase).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
RT derived from a truncated type 2 ribosome-inactivating protein";
RL Plant J. 12:1251-1260 (1997).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; U76524; AAC15886.1; -.
DR HSSP; P02879; 2AAL.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR PROSITE; PS0275; SHIGA RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT POTENTIAL.
FT RIBOSOME INACTIVATING PROTEIN, A CHAIN.
FT RIBOSOME INACTIVATING PROTEIN, B CHAIN.
SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 GN TCS.
 OS Trichosanthin kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 (1)
 RP SEQUENCE FROM N.A.
 RP Yuan H., Wang L., Wang Y., An C., Chen Z.;
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF367252; AAK52960.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR HydroLase; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT CHAIN 24 270
 SQ SEQUENCE 269 AA; 31706 MW; A6D5602549CA5657 CRC64;
 (1)
 Query Match 33.4%; Score 340; DB 10; Length 289;
 Best Local Similarity 39.5%; Pred. No. 6.8e-24;
 Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;
 QY 9 INFTTAGATVQSYNTFIRAVRGRITTTGADVRHEIPVLPNVRVGLPINORFILVELSNHAEL 68
 Db 25 VSRFSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSLPGSQRYALHLTNVADE 81
 QY 69 SVTLALDVNAYVGVYRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
 Db 82 TISVAIDVTNVIYMGVYRAGDTSYFF--NEASATEAAKYVFKDAKRVKVTLPYSGNYERLQ 138
 QY 128 QLAGNLRNIELNGPLEBASALYYSTGGTQPLTARSFIICMISEARFYIEGE 187
 Db 139 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIOSTSEARYKFIEQ 193
 QY 188 MRTRI 192
 Db 194 IGKRV 198
 (1)
 RESULT 10
 Q9LRE3
 ID Q9LRE3 PRELIMINARY; PRT; 247 AA.
 AC Q9LRE3
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
 GN TBK.
 OS Trichosanthin sp. Bac Kan 8-98.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=118182;
 (1)
 RP SEQUENCE FROM N.A.
 RP Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
 RA "Genomic DNA clone for mature typ-1 ribosome-inactivating protein from
 RT Trichosanthin sp. sample 01 Bac Kan 8-98 Vien CNH (Hanoi).";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AB039324; BAA92530.1; -.
 DR HSSP; P09989; IMRJ.
 DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW HydroLase; Toxin.
 FT NON TER 1 247
 FT NON TER 247 247
 SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;
 (1)
 Query Match 33.2%; Score 338; DB 10; Length 247;
 Best Local Similarity 40.0%; Pred. No. 8.5e-24;
 Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;
 QY 9 INFTTAGATVQSYNTFIRAVRGRITTTGADVRHEIPVLPNVRVGLPINORFILVELSNHAEL 68
 Db 2 VSRFSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSLPGSQRYALHLTNVADE 58
 QY 69 SVTLALDVNAYVGVYRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
 Db 59 TISVAIDVTNVIYMGVYRAGDTSYFF--NEASATEAAKYVFKDAKRVKVTLPYSGNYERLQ 115
 QY 128 QLAGNLRNIELNGPLEBASALYYSTGGTQPLTARSFIICMISEARFYIEGE 187
 Db 116 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIOSTSEARYKFIEQ 170
 QY 188 MRTRI 192
 Db 171 IGKRV 175
 (1)
 RESULT 11
 Q41216
 ID Q41216 PRELIMINARY; PRT; 289 AA.
 AC Q41216;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
 GN TRICHOSANTHIN, TCS.
 OS Trichosanthin kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 (1)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94271613; PubMed=8003348;
 RA Zheng H., Wang B., Shaw P., Yeung H.;
 RT "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
 RL I Chuan Heueh Pac 21:42-51(1994).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; S70176; AAB31048.1; -.
 DR HSSP; P09989; IMRJ.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW HydroLase; Toxin.
 SQ SEQUENCE 289 AA; 31650 MW; 286AC14D48BCAL17S CRC64;
 (1)
 Query Match 33.2%; Score 338; DB 10; Length 289;
 Best Local Similarity 39.5%; Pred. No. 1.1e-23;
 Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;
 QY 9 INFTTAGATVQSYNTFIRAVRGRITTTGADVRHEIPVLPNVRVGLPINORFILVELSNHAEL 68
 Db 25 VSRFSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSLPGSQRYALHLTNVADE 81
 QY 69 SVTLALDVNAYVGVYRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
 Db 82 TISVAIDVTNVIYMGVYRAGDTSYFF--NEASATEAAKYVFKDAKRVKVTLPYSGNYERLQ 138

QY 128 QLAGNLRNIELNGPLERAIISALYYSTGGTQPLTARSFICICIMISEARFQIEG 187
 DB 139 TAAGKIRENIPGLPALDSAITLIFYNNAN-----SASALMWLIQSTSEARFYKEIOQ 193
 QY 188 MRTRI 192
 DB 194 IGRV 198

RESULT 12
 Q38760 PRELIMINARY; PRT; 252 AA.
 AC Q38760
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (fragment).
 GN RIP.
 OS Abrus precatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 OC NCBI_TaxID=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91201329; PubMed=2016300;
 RX Evenesen G., Mathiesen A., Sundan A.;
 RA "Direct molecular cloning and expression of two distinct abrin A-
 RT chains.";
 RT J. Biol. Chem. 266:6848-6852 (1991).
 RL CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
 CC PROTEINS. BELONGS TO TYPE 2 RIP.
 DR EMBL; X54872; CAA38654.1; -;
 DR HSP; P11140; IABR.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
 FT CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).
 FT NON TER 252
 SQ SEQUENCE 252 AA; 28309 MW; BBFC46B9E92B5DE CRC64;

Query Match 33.0%; Score 336.5; DB 10; Length 252;
 Best Local Similarity 44.9%; Pred. No. 1.2e-23;
 Matches 83; Conservative 24; Mismatches 69; Indels 9; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRGLPQINORFILVELSNHAEL 68
 DB 6 IKFSTEGATSQYKQFIEALRRLRG--LIHDPVLRDPTVEERNYITVELSNGERE 63
 QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDNOQDEAEI--THLFTDVQNRVYTFAGGNY 128
 DB 64 SIEVGIDVTNAYVWAYRAGSQSYFL---RDAPASASTYLTGTQ-RVSLRFDGSGYGLER 119
 QY 129 LAGNLRNIELNGPLERAIISALYYSTGGTQPLTARSFICICIMISEARFQIEGEM 188
 DB 120 WAHQTRQISLGLQALTAIS---FLRSGASNDEKATLIVIQMASEARFYISNRV 176
 QY 189 RTRIR 193

Db 177 GVSIR 181

RESULT 13

Q945S2 PRELIMINARY; PRT; 563 AA.
 AC Q945S2
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA
 DE N-glycosidase).
 GN AVL.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OC NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Van Damme E.J.M.;
 RT "Characterization and cloning of lectins and ribosome-inactivating
 RT proteins from Sambucus nigra leaves.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL; AF409135; AAL04123.1; -;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN B LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Toxin.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 32.4%; Score 330.5; DB 10; Length 563;
 Best Local Similarity 39.5%; Pred. No. 1.4e-22;
 Matches 75; Conservative 39; Mismatches 61; Indels 15; Gaps 4;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRGLPQINORFILVELSNH 65
 DB 28 YPSVFNLDGAKSATYRDELNLKTKVATGTVEVNGLPVLRRESEVQVKSFRFVLPLTNY 87
 QY 66 AELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQDEAEI--THLFTDVQNRVYTFAGGNY 123
 DB 88 NGNTVTLAVDVTNLYVVFAGNSANSYFF----KDATEVQKSNLFVGTQKN-TLSFTGNY 141
 QY 124 DRLEQAGNLRNIELNGPLERAIISALYYSTGGTQPLTARSFICICIMISEARFQY 183
 DB 142 DNLETAANTRESIELGSPSLDGAITSYHGD-----SVARSLLVVIQWSEARF 194
 QY 184 IEGEMRTRIR 193
 DB 195 IEQEVRRSLQ 204

RESULT 14
 Q8GT32 PRELIMINARY; PRT; 563 AA.
 AC Q8GT32
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein nigrin I precursor
 DE (EC 3.2.2.22).
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 32.0534 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVRQYPIINTAGATVQS.....ARFQYIEGEMTRINRYNRS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Jun03:*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	950	98.4	267 13 AAR30722	Ricin A from pIC11
2	950	98.4	267 21 AAB19265	Amino acid sequenc
3	941	97.5	267 14 AAR37290	Ricin A chain. Un
4	941	97.5	267 16 AAR63902	Ricin A-chain (RTA
5	941	97.5	290 18 AAW25136	Ricin A-chain ribo
6	941	97.5	290 18 AAW21699	Ricin A-chain RIP.
7	941	97.5	332 8 AAP70097	Ricin A. Escheric
8	941	97.5	332 8 AAR70838	Sequence of Ricinu
9	941	97.5	332 10 AAP95639	Ricin A encoded by

10	941	97.5	554 16 AAR70827	Anti-cataract immu
11	941	97.5	562 10 AAP50079	Ricin D. Ricinus
12	941	97.5	565 6 AAP50166	Sequence of prepro
13	941	97.5	565 22 AAG78300	Castor bean prepro
14	941	97.5	565 22 AAG78304	Modified castor be
15	941	97.5	576 8 AAP70326	Sequence of Ricinu
16	941	97.5	576 18 AAW25787	Castorbean ricin.
17	941	97.5	576 20 AAY55892	Castor bean ricin
18	941	97.5	576 21 AAY78592	Ricinus communis r
19	941	97.5	576 22 AAG78301	Castor bean prepro
20	941	97.5	576 22 AAG78302	Castor bean prepro
21	937	97.1	200 9 AAP80164	Biosynthetic multi
22	936	97.0	565 7 AAP60240	Preproricin. Ric
23	934	96.8	268 14 AAR39570	Sequence of ricin-
24	934	96.8	574 8 AAP70325	Sequence of Ricinu
25	932	96.6	574 10 AAP94793	DNA sequence of ri
26	931	96.4	534 14 AAR39571	Sequence of G-FIT.
27	930	96.4	332 11 AAR06554	Ricin A gene produ
28	927	96.1	267 14 AAR32430	Ricin A. Syntheti
29	924	95.8	267 16 AAR74176	Ricin A chain (RTA
30	851.5	88.2	540 18 AAW25143	Castor oil plant a
31	851.5	88.2	540 18 AAW21706	R. communis agglut
32	791.5	82.0	534 8 AAP70324	Sequence of Ricin
33	718	74.4	280 10 AAP95648	Ricin agglutinin A
34	336	34.8	247 16 AAR67359	Trichosanthin anti
35	336	34.8	247 21 AAY69048	Amino acid sequenc
36	336	34.8	248 11 AAR07518	Synthetic alpha-tr
37	336	34.8	248 13 AAR25573	Mature alpha-Trich
38	336	34.8	267 18 AAW25140	Trichosanthin (a r
39	336	34.8	267 18 AAW21703	Trichosanthin. Tr
40	336	34.8	289 11 AAR07514	Trichosanthin from
41	336	34.8	289 13 AAR25572	Trichosanthin from
42	336	34.8	289 13 AAR29272	Trichosanthin prot
43	336	34.8	289 14 AAR29286	Encodes chinese cu
44	336	34.8	289 15 AAR55129	Alpha-trichosanthi
45	336	34.8	289 18 AAW10468	Chinese cucumber a

ALIGNMENTS

RESULT 1
AAR30722
ID AAR30722 standard; Protein; 267 AA.
XX
AC AAR30722;
XX
DT 25-MAR-2003 (updated)
DT 08-FEB-1993 (first entry)
XX
DE Ricin A from pIC1102.
XX
KW pH; temperature; cultivation; host; soluble.
OS Synthetic.
PN EP501692-A2.
XX
PD 02-SEP-1992.
XX
PF 21-FEB-1992; 92EP-0301466.
XX
PR 26-FEB-1991; 91GB-0003925.
PR 26-FEB-1991; 91GB-0003926.
PR 26-FEB-1991; 91GB-0004016.
(ICIL) IMPERIAL CHEM IND PLC.
(ZENE) ZENeca LTD.
PI Pitton JE, Hockney RC, Kara BV;
XX WPI; 1992-294124/36.
DR N-PSDB; AAQ27876.

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XX PT Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by
XX PT adjusting pH and/or temp. during cultivation to increase yield of
XX PT soluble prod.
XX PS Disclosure; Fig 9; 49pp; English.
XX CC Prepn. of ricin A comprises cultivating a host, including a DNA
XX CC sequence which encodes ricin A, e.g. from pIC1102, in a nutrient
XX CC medium for an initial period at a first pH value which favours growth
XX CC of the host; and cultivation the host for a further period at a pH
XX CC lower than the first pH value, and opt. cooling the host during the
XX CC terminal portion of the cultivation and harvesting the host during
XX CC the terminal portion. By adjusting the pH and temp. during the
XX CC cultivation of hosts, high yields of soluble recombinant ricin A
XX CC are obtained.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 267 AA;

Query Match 98.4%; Score 950; DB 13; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.1e-93;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50
DB 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVREHIEPVLNPRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110
DB 61 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLENIELNGPLEEALISALYYSTGTGTLPTLARSFIIICQMISEAAR 170
DB 121 GNYDRLEQLAGNLENIELNGPLEEALISALYYSTGTGTLPTLARSFIIICQMISEAAR 180
QY 171 FOYIEGEMRTRIRYNRRS 188
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 2
AAB19265
ID AAB19265 standard; protein; 267 AA.
XX AC AAB19265;
XX DT 19-FEB-2001 (first entry)
XX DE Amino acid sequence of a human ricin toxin A chain (RTA).
XX KW Immunotoxin; cytokine; vascular leak syndrome; VLS; lymphoma; myeloma;
XX KW graft versus host disease; metastatic lesion tumour; tumour; immunotoxin;
XX KW ricin toxin A chain.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 74..76
XX FT /note= "vascular leak syndrome (VLS) inducing motif"
XX PN WO200058456-A2.
XX PD 05-OCT-2000.
XX PF 30-MAR-2000; 2000WO-US08600.
XX PR 30-MAR-1999; 99US-0126826.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Vitetta ES, Ghetie VF, Baluna RG, Smallshaw J;

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XX WPI; 2000-664922/64.
XX Modifying the ability of a proteinaceous composition to induce a toxic
XX effect for reducing vascular leak syndrome, comprises identifying at
XX least one specified amino acid sequence and altering it -
XX Example 1; Page 119-120; 125pp; English.
XX The specification describes a method for producing immunotoxins and
XX cytokines with a reduced ability to promote vascular leak syndrome
XX (VLS). The immunotoxins are useful for treating graft versus host
XX disease, non-Hodgkin's and Hodekin's lymphoma, myeloma, metastatic
XX lesion tumours and some type of solid tumours. The present sequence
XX represents an immunotoxin (ricin toxin A chain) which induces VLS.
XX The VLS-inducing motif can be mutated or deleted so that VLS is not
XX induced.
XX SQ Sequence 267 AA;

Query Match 98.4%; Score 950; DB 21; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.1e-93;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50
DB 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVREHIEPVLNPRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110
DB 61 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLENIELNGPLEEALISALYYSTGTGTLPTLARSFIIICQMISEAAR 170
DB 121 GNYDRLEQLAGNLENIELNGPLEEALISALYYSTGTGTLPTLARSFIIICQMISEAAR 180
QY 171 FOYIEGEMRTRIRYNRRS 188
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 3
AAR37290
ID AAR37290 standard; protein; 267 AA.
XX AC AAR37290;
XX DT 25-MAR-2003 (updated)
XX DT 09-JAN-2003 (updated)
XX DT 13-SEP-1993 (first entry)
XX DE Ricin A chain.
XX KW Type II ribosome-inactivating protein; type II RIP; gelonin;
XX KW momordin; immunconjugate; autoimmune disease; cell killing; toxin.
XX OS Unidentified.
XX PN WO9309130-A1.
XX PD 13-MAY-1993.
XX PF 04-NOV-1992; 92WO-US09487.
XX PR 04-NOV-1991; 91US-0787567.
XX PR 19-JUN-1992; 92US-0901707.
XX PA (XOMA ) XOMA CORP.
XX PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX WPI; 1993-167617/20.

```

PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating autoimmune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 XX
 XX Claim 1; Page 92; 163pp; English.

XX The invention covers analogues of Type I RIPs. Ricin is a Type II
 CC RIP whose A chain is homologous to plant type I RIPs. The analogues
 CC of the invention have a cysteine available for intermolecular
 CC disulphide bonding at an amino acid position corresp. to a position
 CC not naturally available for bonding; the cys residue is located in
 CC the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 267 AA;

Query Match 97.5%; Score 941; DB 14; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLTGADVREHIVLPNRVGLPINQRFILVEL 62
 QY 53 SNHAELSVTLALDVTNAYVGYGRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGGN 112
 DB 63 SNHAELSVTLALDVTNAYVGYGRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGGN 122
 QY 113 YDRLEQLAGNLRENIELNGPLERAI SALYYVSTGGTQLPTLARSFFICIQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRENIELNGPLERAI SALYYVSTGGTQLPTLARSFFICIQMISEAARFQ 182
 QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 4
 AAR63902
 ID AAR63902 standard; protein; 267 AA.
 XX AC AAR63902;

DT 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)

DE Ricin A-chain (RTA).

KW Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

OS Ricinus communis.

XX WO9426910-A1.

XX 24-NOV-1994.

XX PF 12-MAY-1994; 94WO-US05348.

XX PR 12-MAY-1993; 93US-0064691.

XX PA (XOMA) XOMA CORP.

XX PI Better MD, Carroll SS, Studnicka GM, Carroll SF;

XX DR WPI; 1995-006804/01.

XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins

PT - which are suitable for use as components of cytotoxic
 PT therapeutic agents.

XX Example 3; Fig 1; 221pp; English.

XX AAR63902 is the ricin A chain gene product, it is analogous to the
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
 CC which include gene fusion products and immunoconjugates. CTAs may
 CC be used to selectively eliminate any cell type to which a RIP
 CC component is targeted, by the specific binding capacity of the
 CC second component of the agent. They can be used in the treatment
 CC of diseases where the elimination of a particular cell type is
 CC desired, such as autoimmune disease, cancer and graft-versus-host
 CC disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 267 AA;

Query Match 97.5%; Score 941; DB 16; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLTGADVREHIVLPNRVGLPINQRFILVEL 62
 QY 53 SNHAELSVTLALDVTNAYVGYGRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGGN 112
 DB 63 SNHAELSVTLALDVTNAYVGYGRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGGN 122
 QY 113 YDRLEQLAGNLRENIELNGPLERAI SALYYVSTGGTQLPTLARSFFICIQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRENIELNGPLERAI SALYYVSTGGTQLPTLARSFFICIQMISEAARFQ 182
 QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 5

AAW25136
 ID AAW25136 standard; protein; 290 AA.

XX AC AAW25136;

DT 25-MAR-2003 (updated)

DT 02-DEC-1997 (first entry)

DE Ricin A-chain ribosome inhibitory protein inactive precursor.

KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley translation inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SUT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.

OS Synthetic.

XX US5646026-A.

XX 08-JUL-1997.

XX PF 07-JUN-1995; 95US-0485286.

XX PR 09-DEC-1992; 92US-0987927.

XX PR 11-JUN-1990; 90US-0535636.

XX PR 26-JAN-1995; 95US-0378761.

XX PR 07-JUN-1995; 95US-0485286.

XX PA (DOWC) DOWELANCO.

XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-362934/33.
 XX PT DNA encoding pro-ribosome inactivating proteins - inactive
 XX PT precursors of ribosome inactivating proteins; can be expressed in
 XX PT eukaryotic cells without causing cell death
 XX
 XX PS Claim 4; Column 91-94; 186pp; English.
 XX
 XX AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
 CC Saporin. The RIPs can be used in the construction of therapeutic
 CC toxins targeted to specific cells such as tumour cells via the
 CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.
 CC A further use is in HIV therapy (see US4869903). There is interest
 CC in expressing RIP recombinantly in host eukaryotic cells, because of
 CC the capacity to provide correct post-translational processing. However,
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to
 CC eukaryotic cells, they can be recombinantly expressed in such cells and
 CC then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX SQ Sequence 290 AA;
 Query Match 97.5%; Score 941; DB 18; Length 290;
 Best Local Similarity 94.9%; Pred. No. 1.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 27 PKQYPIINFATTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILVEL 86
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 112
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 146
 QY 113 YDRLEQLAGNLRENIELNGPLEEASALYYSTGGTQPLTLARSFTICQIMISEARFQ 172
 Db 147 YDRLEQLAGNLRENIELNGPLEEASALYYSTGGTQPLTLARSFTICQIMISEARFQ 206
 QY 173 YIEGEMTRIRYNRS 188
 Db 207 YIEGEMTRIRYNRS 222
 RESULT 6
 AAW21699
 ID AAW21699 standard; Protein; 290 AA.
 AC
 AC AAW21699;
 XX
 XX 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 XX Ricin A-chain RIP.
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX
 OS Ricinus communis.
 XX
 XX Key Location/Qualifiers
 FH Region 152..162
 FT

FT FT /note= "Position of possible insertion of internal
 XX XX peptide linker sequence"
 PN US5635384-A.
 XX
 PD 03-JUN-1997.
 XX
 PF 26-JAN-1995; 95US-0378761.
 XX
 PR 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 PR (DOWC) DOWELANCO.
 PA Hey TD, Morgan AER, Walsh TA;
 PI WPI; 1997-309831/28.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 XX Claim 2; Column 91-94; 121pp; English.
 XX
 CC The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the
 CC proRIP of the invention. The proRIP has a selectively removable,
 CC internal peptide linker. The precursor sequence is incapable of
 CC inactivating eukaryotic ribosomes, but can be converted by removal
 CC of the linker into a protein having alpha and beta fragments and being
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent
 CC inhibitors of eukaryotic protein synthesis. They possess a highly
 CC specific N-glycosidase activity which cleaves the glycosidic bond of
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T
 CC cells. The inactive proRIP proteins make it possible to provide protein
 CC synthesis inhibitors with uses in practical and improved ways not before
 CC possible. The RIP can be used to make cytotoxic conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX SQ Sequence 290 AA;
 Query Match 97.5%; Score 941; DB 18; Length 290;
 Best Local Similarity 94.9%; Pred. No. 1.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 27 PKQYPIINFATTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILVEL 86
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 112
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 146
 QY 113 YDRLEQLAGNLRENIELNGPLEEASALYYSTGGTQPLTLARSFTICQIMISEARFQ 172
 Db 147 YDRLEQLAGNLRENIELNGPLEEASALYYSTGGTQPLTLARSFTICQIMISEARFQ 206
 QY 173 YIEGEMTRIRYNRS 188
 Db 207 YIEGEMTRIRYNRS 222
 RESULT 7
 AAW70097
 ID AAW70097 standard; protein; 332 AA.
 XX
 XX AAP70097;
 XX
 XX 09-APR-1991 (first entry)
 DT
 XX Ricin A.

```

XX Ricin A; Met-aminopeptidase.
KW Escherichia coli.
XX EP129237-A.
XX PD 22-APR-1987.
XX PF 19-SEP-1986; 86EP-0307242.
XX PR 06-MAY-1986; 86US-0860330.
XX FR 20-SEP-1985; 85US-0778414.
XX PA (CETU ) CETUS CORP.
XX PI Benbassat A, Bauer KA, Chang S, Chang SY;
XX WPI; 1987-110172/16.
XX DR N-PSDB; AAN70152.
XX PT N-terminal methionine free proteins prodn. - by using host
XX transformed with vector to express a methionine-amino-peptidase
XX PS Disclosure; Fig. 4; 20pp; English.
XX CC Ricin A may be produced in a form which lacks an N-terminal Met
XX using Met-aminopeptidase from E.coli.
XX SQ Sequence 332 AA;
Query Match 97.5%; Score 941; DB 8; Length 332;
Best Local Similarity 94.9%; Pred. No. 1.4e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSNTNFIRAVRGRLT-----VLPNRVGLPINOREILVEL 52
DB 38 PKQYPIINFTTAGATVQSNTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINOREILVEL 97
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 157
QY 113 YDRLEQLAGNLRENIELGNGPLEEALISALYYSTGGTOLPTLARSFFIICIMISEARFQ 172
DB 158 YDRLEQLAGNLRENIELGNGPLEEALISALYYSTGGTOLPTLARSFFIICIMISEARFQ 217
QY 173 YIEGEMRTRIRYNRRS 188
DB 218 YIEGEMRTRIRYNRRS 233
RESULT 8
ID AAP70838
XX AAP70838 standard; protein; 332 AA.
XX AC AAP70838;
XX DT 25-MAR-2003 (updated)
XX DT 18-FEB-1991 (first entry)
XX DE Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
XX DE A protein encoded by PRA123.
XX KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
XX plant toxin.
XX OS Ricinus communis.
XX FH Key
XX FT Region
XX FT Location/Qualifiers
XX FT 1..32
XX FT /note="Leader"
XX FT 33..302

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FT FT /note="A-chain"
FT FT 315..332
FT FT /note="B-chain"
XX EP237676-A.
XX PD 23-SEP-1987.
XX PF 13-NOV-1986; 86EP-0308877.
XX PR 07-MAR-1986; 86US-0837583.
XX PA (CETU ) CETUS CORP.
XX PA (CHIR ) CHIRON CORP.
XX PI Piatak M;
XX WPI; 1987-265177/38.
XX DR N-PSDB; AAN70519.
XX PT New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX by recombinant DNA procedures with specific isolation steps for
XX purer and soluble prods.
XX PS Disclosure; Fig 1; 112pp; English.
XX CC The full-length sequences encoding ricin A (AAN70520), ricin D
XX (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
XX form were obtd. using messenger RNA to obtain a cDNA library, and
XX then probing the library to retrieve the desired cDNA inserts. The
XX library was probed using the 35-mer given in AAN70514. Figure 4 (see
XX AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
XX plasmids contg. cDNA inserts obtd. by probing a cDNA library for
XX sequences encoding ricin B using the probe in AAN70517. The cDNA
XX inserts can be placed into expression vectors. Site-directed
XX mutagenesis may be used to place an ATG start codon and a HindIII
XX site at the beginning of the mature protein (see AAN70518). The
XX coding sequences of the inserts can be ligated into expression
XX vectors contg. the PhOA promoter-operator and leader sequence
XX (AAN70523) and suitable retroregulators.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 332 AA;
Query Match 97.5%; Score 941; DB 8; Length 332;
Best Local Similarity 94.9%; Pred. No. 1.4e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSNTNFIRAVRGRLT-----VLPNRVGLPINOREILVEL 52
DB 38 PKQYPIINFTTAGATVQSNTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINOREILVEL 97
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 157
QY 113 YDRLEQLAGNLRENIELGNGPLEEALISALYYSTGGTOLPTLARSFFIICIMISEARFQ 172
DB 158 YDRLEQLAGNLRENIELGNGPLEEALISALYYSTGGTOLPTLARSFFIICIMISEARFQ 217
QY 173 YIEGEMRTRIRYNRRS 188
DB 218 YIEGEMRTRIRYNRRS 233
RESULT 9
ID AAP95639
XX AAP95639 standard; protein; 332 AA.
XX AC AAP95639;
XX DT 25-MAR-2003 (updated)
XX DT 31-OCT-2002 (updated)

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DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 XX Ricinus communis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..35
 FT /label= leader sequence
 FT Peptide 36..302
 FT /label=A-chain
 FT Peptide 303..314
 FT /label=linker
 FT Peptide 315..332
 FT /label=B-chain
 XX EP335476-A.
 PN 04-OCT-1989.
 XX 19-JAN-1989; 89EP-0201162.
 XX 08-FEB-1984; 84US-0578115.
 PR 08-FEB-1984; 84US-0578121.
 PR 08-FEB-1984; 84US-0578122.
 PR 07-SEP-1984; 84US-0648759.
 PR 20-SEP-1984; 84US-0653515.
 XX (CETU) CETUS CORPORATION.
 PA Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Platak NJ;
 PI WPI; 1989-286959/40.
 DR N-PSDB; AAN91281.
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 PT high cell specificity and good extracellular stability.
 XX Disclosure; Fig 14; 54pp; English.
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 332 AA;
 SQ
 Query Match 97.5%; Score 941; DB 10; Length 332;
 Best Local Similarity 94.9%; Pred. NO. 1.4e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVDRHEIPVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAELSVTLALDVNTAYVGVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 112
 DB 98 SNHAELSVTLALDVNTAYVGVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 157
 QY 113 YDRLEQAGNIRELNGNPLEEAIISALYYSTGCTGTPILARSFFIICMISEARFQ 172
 DB 158 YDRLEQAGNIRELNGNPLEEAIISALYYSTGCTGTPILARSFFIICMISEARFQ 217

QY 173 YIEGEMRTRIRYNRRS 188
 DB 218 YIEGEMRTRIRYNRRS 233
 RESULT 10
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX AAR70827;
 XX 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX Anti-cataract immunotoxin.
 XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW pHB19; 4197X; monoclonal antibody; MAB.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..27
 FT /label= Sig_peptide
 FT /note= "phoA signal sequence"
 FT Domain 28..145
 FT /label= HEAVY
 FT Peptide 148..166
 FT /note= "MAB 4197X heavy chain"
 FT /label= LINKER
 FT Domain 169..274
 FT /label= LIGHT
 FT /note= "MAB 419X light chain"
 FT Domain 276..544
 FT /label= RICIN-A
 FT Peptide 549..554
 FT /label= TAG
 FT /note= "hexa-histidine tail"
 XX MO9503828-A1.
 XX 09-FEB-1995.
 XX 15-JUL-1994; 94WO-US07919.
 XX 02-AUG-1993; 93US-0101329.
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 XX WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.
 XX Disclosure; Fig.4; 68pp; English.
 XX The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium IgG3 MAB 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from pHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 554 AA;
 SQ
 Query Match 97.5%; Score 941; DB 16; Length 554;
 Best Local Similarity 94.9%; Pred. NO. 2.7e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 280 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPVLPNRVGLPINQRFILVEL 339
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGFN 112
 DB 340 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGFN 399
 QY 113 YDRLEQLAGNLRNLELGNGLPLEEASIALYVYSTGGTQLTPTLARSFIICQMISEAARFQ 172
 DB 400 YDRLEQLAGNLRNLELGNGLPLEEASIALYVYSTGGTQLTPTLARSFIICQMISEAARFQ 459
 QY 173 YIEGEMRTRIRYNRRS 188
 DB 460 YIEGEMRTRIRYNRRS 475

RESULT 11
 AAP90079
 ID AAP90079 standard; protein; 562 AA.
 XX AC
 XX AAP90079;
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX Ricin D.
 DE Ricin D; Ricinus communis; castor beans; Zanicariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX Ricinus communis (castor beans).
 OS
 XX WO8904839-A.
 PN 01-JUN-1989.
 PD 23-NOV-1988; 88WO-US04238.
 PF 24-NOV-1987; 87US-0124735.
 PR (GEMY) GENETICS INST INC.
 XX Brown EL, Jones S;
 PI WPI; 1989-178366/24.
 DR N-PSDB; AAN90068.
 XX Modified ricin molecules and toxin conjugates
 PT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 XX Disclosure; fig 1; 51pp; English.
 XX Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 562 AA;
 SQ

Query Match 97.5%; Score 941; DB 10; Length 562;
 Best Local Similarity 94.9%; Pred. No. 2.8e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGFN 112

DB 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGFN 157
 QY 113 YDRLEQLAGNLRNLELGNGLPLEEASIALYVYSTGGTQLTPTLARSFIICQMISEAARFQ 172
 DB 158 YDRLEQLAGNLRNLELGNGLPLEEASIALYVYSTGGTQLTPTLARSFIICQMISEAARFQ 217
 QY 173 YIEGEMRTRIRYNRRS 188
 DB 218 YIEGEMRTRIRYNRRS 233

RESULT 12
 AAP50166
 ID AAP50166 standard; Protein; 565 AA.
 XX AC
 XX AAP50166;
 DT 16-OCT-1991 (first entry)
 XX Sequence of preprorin encoded by pRCL617.
 DE Toxin; anti-tumour therapy.
 XX Ricinus.
 OS
 XX Key
 FH Peptide Location/Qualifiers
 FT 1..24 /label= signal
 FT Protein 25..565
 FT Region 292..303
 FT /label= links the C-terminus of the A chain and
 FT the N-terminus of the B chain
 FT Modified-site 34..36
 FT /label= N-linked glycosylation
 FT Modified-site 260..262
 FT /label= N-linked glycosylation
 FT Modified-site 398..400
 FT /label= N-linked glycosylation
 FT Modified-site 438..440
 FT /label= N-linked glycosylation
 XX EP145111-A.
 XX 19-JUN-1985.
 XX 13-JUL-1984; 84EP-0304801.
 XX 13-MAR-1984; 84GB-0006569.
 XX 15-JUL-1983; 83GB-0019265.
 XX 15-JUL-1983; 83CH-0019265.
 XX (UYWA-) UNIV WARWICK.
 XX Lord JM, Roberts LM, Lamb FI;
 XX WPI; 1985-148040/25.
 XX N-PSDB; AAN50202.
 XX New DNA sequences coding for ricin type plant toxin - or its
 PT mutants, and modified vectors and host microorganisms
 PS Disclosure; Page 30-30c; 40pp; English.
 XX Preprorin is the whole polypeptide encoded by AAN50202 and the DNA
 CC encoding this is claimed. Preprorin is obtained from preprorin by
 CC removal of the AA leader sequence. The linker AA sequence which is
 CC present in the precursor polypeptide is enzymatically removed in the
 CC cell to separate the A and B chains, which are joined by a
 CC disulphide bridge during the formation of the ricin molecule itself.
 CC This linker region as well as the presumptive amino terminal leader
 CC or signal sequence are not present in the sequences already
 CC published by Funatsu et al.

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XX SQ Sequence 565 AA;
Query Match 97.5%; Score 941; DB 6; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHRDIPVLPNRVGLPINQRFILVEL 86
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 146
QY 113 YDRLEQLAGNLRENIELGNGPLEEAISSALYYSTGTQPLTARSFFIICIMISEARFQ 172
Db 147 YDRLEQLAGNLRENIELGNGPLEEAISSALYYSTGTQPLTARSFFIICIMISEARFQ 206
QY 173 YIEGEMTRIRYNRRS 188
Db 207 YIEGEMTRIRYNRRS 222

RESULT 13
AAG78300
ID AAG78300 standard; Protein; 565 AA.
AC AAG78300;
DT 15-NOV-2001 (first entry)
DE Castor bean preprorin protein (SEQ ID 1).
KW Castor bean plant; preprorin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide activity; viral protease.
OS Ricinus communis.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal peptide
FT Protein /label= Ricin_A_chain
FT Peptide /note= "N-glycosidase"
FT Peptide 291..302
FT Protein /label= Linker_peptide
FT Protein /note= "Cleaved during activation of ricin"
FT Protein 303..565
FT Protein /label= Ricin_B_chain
FT Protein /note= "Galactose/N-acetylgalactosamine-binding lectin"
XX
PN WO200160393-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US05282.
XX
PR 16-FEB-2000; 2000US-0182759.
XX
PA (BECH-) BECHTEL BWXT IDAHO LLC.
XX
PI Keener WK, Ward TE;
XX
DR WPI; 2001-581908/65.
DR N-PSDB; AAI64137.
XX
PT Novel composition comprising toxin e.g., ricin based antiviral compound
PT useful for treating viral infections such as human immunodeficiency
PT virus infection.
XX
PS Disclosure; Page 47-50; 66pp; English.

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XX The sequence relates to preprorin protein encoded by the DNA sequence
CC given in AAI64137. The invention relates to a novel toxin (e.g., ricin)
CC based antiviral agent which is toxic to virus-infected cells, but
CC non-toxic to uninfected cells. The invention has anti-HIV and virucide
CC activities. Its mechanism of action is through inactivation of cellular
CC ribosomes and enhancement of binding of the antiviral agent to galactose
CC residues on cell surfaces, and its cellular internalisation. The
CC invention is useful for treating human immunodeficiency virus infection
CC and other viral infections, especially retroviral infections. The
CC antiviral agent is activated in viral particles or early-stage infected
CC cells, killing the cells upon infection and effectively preventing the
CC integration of the viral genome into the host genome thereby preventing
CC the latency/rebound problem. The agent enters all HIV susceptible cells,
CC and not just cells known to act as host cells for the virus. The
CC antiviral agent remains inert in a cell until degraded in it, unless the
CC cell is infected with the virus, where the viral protease activates it.
XX
SQ Sequence 565 AA;
Query Match 97.5%; Score 941; DB 22; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHRDIPVLPNRVGLPINQRFILVEL 86
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 146
QY 113 YDRLEQLAGNLRENIELGNGPLEEAISSALYYSTGTQPLTARSFFIICIMISEARFQ 172
Db 147 YDRLEQLAGNLRENIELGNGPLEEAISSALYYSTGTQPLTARSFFIICIMISEARFQ 206
QY 173 YIEGEMTRIRYNRRS 188
Db 207 YIEGEMTRIRYNRRS 222

RESULT 14
AAG78304
ID AAG78304 standard; Protein; 565 AA.
AC AAG78304;
DT 27-NOV-2001 (first entry)
DE Modified castor bean preprorin (SEQ ID 10).
KW Castor bean plant; preprorin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide; viral protease.
XX
OS Chimeric - Ricinus communis
OS Chimeric - Human immunodeficiency virus type 2.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal_peptide
FT Protein 25..565
FT Protein /label= Prorin
FT Protein /note= "Prorin consists of the ricin A chain, a linker
FT peptide, and the ricin B chain. Prorin is
FT proteolytically cleaved between the A chain and
FT the linker to yield mature ricin"
XX
FT Protein 25..291
FT Protein /label= Ricin_A_chain
FT Protein /note= "N-glycosidase"
FT Peptide 292..303
FT Peptide /label= Linker_peptide
FT Cleavage-site 296..297

```

FT Protein /label= HIV_protease_cleavage_site
 FT 344..565
 FT /label= Ricin B chain
 FT /note= "Galactose/N-acetylglucosamine-binding lectin"
 PN WO200160393-A1.
 XX 23-AUG-2001.
 XX 15-FEB-2001; 2001WO-US05282.
 XX 16-FEB-2000; 2000US-0182759.
 XX (BECH-) BECHTEL BMX IDAHO LLC.
 XX Keener WK, Ward TE;
 XX WPI; 2001-581908/65.
 XX N-PSDB; AAI64145.
 XX Novel composition comprising toxin e.g., ricin based antiviral compound
 PT useful for treating viral infections such as human immunodeficiency
 FT virus infection.
 XX Example 1; Page 59-63; 66pp; English.
 XX The sequence relates to the amino acid sequence of a modified prepropricin
 CC protein encoded by AAI64145. The invention relates to a novel toxin
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected
 CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
 CC virucide activities. The agent is able to enter all HIV susceptible
 CC cells, and not just cells known to act as host cells for the virus. The
 CC antiviral agent remains inert in a cell unless the cell is infected
 CC with the HIV virus, where the viral protease activates it. Ricin's
 CC mechanism of action is through inactivation of cellular ribosomes and
 CC enhancement of binding of the antiviral agent to galactose residues on
 CC cell surfaces, and its cellular internalisation. The invention is useful
 CC for treating human immunodeficiency virus infection and other viral
 CC infections, especially retroviral infections. The antiviral agent is
 CC activated in viral particles or early-stage infected cells, killing the
 CC cells upon infection and effectively preventing the integration of the
 CC viral genome into the host genome thereby preventing the latency/rebound
 CC problem.
 XX SQ Sequence 565 AA;
 Query Match 97.5%; Score 941; DB 22; Length 565;
 Best Local Similarity 94.9%; Pred. No. 2.8e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 Db 27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 86
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 146
 QY 113 YDRLEQAGLNRENIELGNGPLEEASALYYVSTGGTQLPRLARSFIICQMISEAARFQ 172
 Db 147 YDRLEQAGLNRENIELGNGPLEEASALYYVSTGGTQLPRLARSFIICQMISEAARFQ 206
 QY 173 YIEGEMRTRIRYNRS 188
 Db 207 YIEGEMRTRIRYNRS 222
 RESULT 15
 AAP70326
 ID AAP70326 standard; Protein; 576 AA.
 XX
 AC AAP70326;
 XX

DT 25-MAR-2003 (updated)
 DT 21-MAY-1991 (first entry)
 XX
 DE Sequence of Ricinus communis (castor bean) Ricin toxin
 DE (RT or ricin) E precursor encoded by PRT38.
 XX
 KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
 KW plant toxin.
 XX
 OS Ricinus communis.
 XX
 FH Key Location/Qualifiers
 FT Region 1..35
 FT /note= "leader"
 FT Region 36..302
 FT /note= "A-chain"
 FT Region 315..576
 FT /note= "B-chain"
 XX
 PN EP237676-A.
 XX
 XX 23-SEP-1987.
 XX
 XX 13-NOV-1986; 86EP-0308877.
 XX
 XX 07-MAR-1986; 86US-0837583.
 XX
 XX (CETU) CETUS CORP.
 XX (CHIR) CHIRON CORP.
 XX
 XX Piatak M;
 XX
 DR WPI; 1987-265177/38.
 DR N-PSDB; AAN70526.
 XX
 XX New non-glycosylated ricin precursor and toxin etc. - are prepd.
 PT by recombinant DNA procedures with specific isolation steps for
 XX purer and soluble prods.
 XX
 PS Disclosure; Fig 14(1-2); 112pp; English.
 XX
 XX The full length sequences encoding ricin A (AAN70520), ricin D
 CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
 CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three
 CC plasmids containing cDNA inserts obtained by probing a cDNA library
 CC for sequences encoding ricin B using the probe in AAN70517. The cDNA
 CC inserts can be placed into expression vectors. Site-directed
 CC mutagenesis may be used to place an ATG start codon and a HindIII
 CC site at the beginning of the mature protein, (see AAN70518). The
 CC coding sequences of the inserts can be ligated into expression
 CC vectors containing the PhOA promoter-operator and leader sequence
 CC (AAN70523) and suitable retroregulators.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 576 AA;
 Query Match 97.5%; Score 941; DB 8; Length 576;
 Best Local Similarity 94.9%; Pred. No. 2.9e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 Db 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
 Db 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 157
 QY 113 YDRLEQAGLNRENIELGNGPLEEASALYYVSTGGTQLPRLARSFIICQMISEAARFQ 172

Db 158 YDRLEQLAGNLRNIELGNGPLEEASALYYSTGGTOLPTLARSFFICIMISEAARFQ 217

Qy 173 YIEGEMRTRIRYNRRS 188

|||||

Db 218 YIEGEMRTRIRYNRRS 233

Search completed: February 10, 2004, 16:22:28
Job time : 33.0534 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 33.9288 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-5
Perfect score: 1025
Sequence: 1 MIFPKQYPIINFTAGATVQ.....ARFQYIEGEMTRIRYNRRS 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_19Jun03:*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	99.5	267	14	AAAR37290
2	1020	99.5	267	16	AAAR37290
3	1020	99.5	290	18	AAW251136
4	1020	99.5	290	18	AAW21699
5	1020	99.5	332	8	AAAP70097
6	1020	99.5	332	8	AAAP70838
7	1020	99.5	332	10	AAAP95639
8	1020	99.5	554	16	AAAR70827
9	1020	99.5	562	10	AAAP90079

10	1020	99.5	565	22	AAAG78304	Modified castor be
11	1020	99.5	576	8	AAAP70326	Sequence of Ricinu
12	1020	99.5	576	18	AAW25787	Castor bean ricin.
13	1020	99.5	576	20	AAAY55892	Castor bean ricin
14	1020	99.5	576	21	AAAY78592	Ricinus communis r
15	1020	99.5	576	22	AAAG78301	Castor bean prepro
16	1020	99.5	576	22	AAAG78302	Castor bean prepro
17	1018	99.3	268	14	AAAR39570	Sequence of ricin-
18	1017	99.2	565	6	AAAP50166	Sequence of prepro
19	1017	99.2	565	22	AAAG78300	Castor bean prepro
20	1016	99.1	200	9	AAAP80164	Biosynthetic multi
21	1015	99.0	534	14	AAAR39571	Sequence of G-FIT.
22	1013	98.8	574	8	AAAP70325	Sequence of Ricinu
23	1012	98.7	565	7	AAAP60240	Preproricin. Ricin
24	1011	98.6	574	10	AAAP94793	DNA sequence of ri
25	1010	98.5	267	13	AAAR30722	Ricin A from pIC11
26	1010	98.5	267	11	AAAB19265	Amino acid sequenc
27	1009	98.4	332	11	AAAR06554	Ricin A gene produ
28	993	96.9	267	16	AAAR74176	Ricin A chain (RTA
29	987	96.3	267	14	AAAR32430	Ricin A. Syntheti
30	930.5	90.8	540	18	AAW25143	Castor oil plant a
31	930.5	90.8	540	18	AAW21706	R. communis agglut
32	796.5	77.7	534	8	AAAP70324	Sequence of Ricin
33	778	75.9	280	10	AAAP95648	Ricin agglutinin A
34	342	33.4	247	16	AAAR67359	Trichosanthin anti
35	342	33.4	247	21	AAAY63048	Amino acid sequenc
36	342	33.4	248	11	AAAR07518	Synthetic alpha-tr
37	342	33.4	248	13	AAAR25573	Mature alpha-trich
38	342	33.4	267	18	AAW25140	Trichosanthin (a r
39	342	33.4	267	18	AAW21703	Trichosanthin. Tr
40	342	33.4	289	11	AAAR07514	Trichosanthin from
41	342	33.4	289	13	AAAR25572	Trichosanthin prot
42	342	33.4	289	13	AAAR29272	Encodes chinese cu
43	342	33.4	289	14	AAAR32986	Alpha-trichosanthi
44	342	33.4	289	15	AAAR55129	Chinese cucumber a
45	342	33.4	289	18	AAW10468	

ALIGNMENTS

RESULT 1
AAAR37290
ID AAAR37290 standard; protein; 267 AA.
XX
XX AAAR37290;
AC
AC
XX
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 13-SEP-1993 (first entry)
XX
XX Ricin A chain.
DE
XX
XX Type II ribosome-inactivating protein; type II RIP; gelonin;
XX memordin; immunoconjugate; autoimmune disease; cell killing; toxin.
XX
XX Unidentified.
OS
XX
XX WO9309130-A1.
XX
XX 13-MAY-1993.
XX
XX 04-NOV-1992; 92WO-US09487.
XX
XX 04-NOV-1991; 91US-0787567.
XX 19-JUN-1992; 92US-0901707.
XX
XX (XOMA) XOMA CORP.
XX
XX Escheric
PI Ricin A encoded by
XX Anti-catact immu
DR WPI; 1993-167617/20.
XX

PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating auto immune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 XX
 PS Claim 1; Page 92; 163pp; English.
 XX
 CC The invention covers analogues of Type I RIPs. Ricin is a Type II
 CC RIP whose A chain is homologous to plant type I RIPs. The analogues
 CC of the invention have a cysteine available for intermolecular
 CC disulphide bonding at an amino acid position corresp. to a position
 CC not naturally available for bonding; the cys residue is located in
 CC the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 267 AA;

Query Match 99.5%; Score 1020; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHVPVLPNRVGLPINQRFILV 61
 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHVPVLPNRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
 QY 122 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMRTIRYNRRS 199
 DB 181 FOYIEGEMRTIRYNRRS 198

RESULT 2
 AAR63902
 ID AAR63902 standard; protein; 267 AA.

XX AAR63902;
 XX
 XX 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)
 DT
 XX Ricin A-chain (RTA).
 DE
 XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX Ricinus communis.
 OS
 XX WO9426910-A1.
 PN
 XX 24-NOV-1994.
 PD
 XX 12-MAY-1994; 94WO-US05348.
 PF
 XX 12-MAY-1993; 93US-0064691.
 PR (XOMA) XOMA CORP.
 XX
 XX Better MD, Carroll SS, Studnicka GM, Carroll SF;
 PI WPI; 1995-006804/01.
 DR
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins
 PT

PT - which are suitable for use as components of cytotoxic
 PT therapeutic agents.

XX Example 3; Fig 1; 221pp; English.

XX
 CC AAR63902 is the ricin A chain gene product, it is analogous to the
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
 CC which include gene fusion products and immunoconjugates. CTAs may
 CC be used to selectively eliminate any cell type to which a RIP
 CC component is targeted, by the specific binding capacity of the
 CC second component of the agent. They can be used in the treatment
 CC of diseases where the elimination of a particular cell type is
 CC desired, such as autoimmune disease, cancer and graft-versus-host
 CC disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 267 AA;

Query Match 99.5%; Score 1020; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHVPVLPNRVGLPINQRFILV 61
 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHVPVLPNRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
 QY 122 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMRTIRYNRRS 199
 DB 181 FOYIEGEMRTIRYNRRS 198

RESULT 3

AAR63902
 ID AAR63902 standard; protein; 290 AA.

XX AAR63902;
 XX
 XX 25-MAR-2003 (updated)
 DT 02-DEC-1997 (first entry)
 DT
 XX Ricin A-chain ribosome inhibitory protein inactive precursor.
 DE
 XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SUT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.
 OS
 XX Synthetic.
 XX
 XX US5646026-A.
 PN
 XX 08-JUL-1997.
 PD
 XX 07-JUN-1995; 95US-0485286.
 PF
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX
 XX (DOWC) DOWELANCO.

XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-362934/33.
 XX
 XX DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 PS Claim 4; Column 91-94; 186pp; English.
 XX
 XX AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
 CC Saporin. The RIPs can be used in the construction of therapeutic
 CC toxins targeted to specific cells such as tumour cells via the
 CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.
 CC A further use is in HIV therapy (see US4869903). There is interest
 CC in expressing RIP recombinantly in host eukaryotic cells, because of
 CC the capacity to provide correct post-translational processing. However,
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to
 CC eukaryotic cells, they can be recombinantly expressed in such cells and
 CC then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 290 AA;
 SQ

Query Match 99.5%; Score 1020; DB 18; Length 290;
 Best Local Similarity 100.0%; Pred. No. 3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61
 DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 84
 QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 DB 85 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 144
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 4
 AAW21699
 ID AAW21699 standard; Protein; 290 AA.
 XX
 AC AAW21699;
 XX
 XX 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 XX Ricin A-chain RIP.
 XX
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX
 OS Ricinus communis.
 XX
 XX Key Location/Qualifiers
 FH 152..162
 FT Region

FT /note= "Position of possible insertion of internal
 FT peptide linker sequence"
 XX
 XX US5635384-A.
 XX
 XX 03-JUN-1997.
 XX
 XX 26-JAN-1995; 95US-0378761.
 XX
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX (DOMC) DOWELANCO.
 XX Hey TD, Morgan AER, Walsh TA;
 WPI; 1997-309831/28.
 PS
 PS Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 PS Claim 2; Column 91-94; 121pp; English.
 CC The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the
 CC proRIP of the invention. The proRIP has a selectively removable,
 CC internal peptide linker. The precursor sequence is incapable of
 CC inactivating eukaryotic ribosomes, but can be converted by removal
 CC of the linker into a protein having alpha and beta fragments and being
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent
 CC inhibitors of eukaryotic protein synthesis. They possess a highly
 CC specific N-glycosidase activity which cleaves the glycosidic bond of
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T
 CC cells. The inactive proRIP proteins make it possible to provide protein
 CC synthesis inhibitors with uses in practical and improved ways not before
 CC possible. The RIP can be used to make cytotoxic conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 290 AA;
 Query Match 99.5%; Score 1020; DB 18; Length 290;
 Best Local Similarity 100.0%; Pred. No. 3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61
 DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 84
 QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 DB 85 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 144
 QY 122 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAR 181
 DB 145 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAR 204
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 5
 AAP70097
 ID AAP70097 standard; protein; 332 AA.
 XX
 AC AAP70097;
 XX
 XX 09-APR-1991 (first entry)
 XX
 DE Ricin A.

```

XX KW Ricin A; Met-aminopeptidase.
XX OS Escherichia coli.
XX PN EP219237-A.
XX PD 22-APR-1987.
XX PF 19-SEP-1986; 86EP-0307242.
XX PR 06-MAY-1986; 86US-0860330.
XX PR 20-SEP-1985; 85US-0778414.
XX PA (CETU ) CETUS CORP.
XX PI Benbassat A, Bauer KA, Chang S, Chang SY;
XX WPI; 1987-110172/16.
XX DR N-PSDB; AAN70152.
XX PT N-terminal methionine free proteins prodn. - by using host
XX PT transformed with vector to express a methionine-amino-peptidase
XX PS Disclosure; Fig. 4; 20pp; English.
XX CC Ricin A may be produced in a form which lacks an N-terminal Met
XX CC using Met-aminopeptidase from E.coli.
XX SQ Sequence 332 AA;
    Query Match 99.5%; Score 1020; DB 8; Length 332;
    Best Local Similarity 100.0%; Pred. No. 3.6e-100;
    Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNVRGLPINQRFILV 61
Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNVRGLPINQRFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 121
Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 155
QY 122 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQIMISEAR 181
Db 156 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQIMISEAR 215
QY 182 FOYIEGEMTRIRYNRRS 199
Db 216 FOYIEGEMTRIRYNRRS 233
RESULT 6
AAP70838
ID AAP70838 standard; protein; 332 AA.
XX AC AAP70838;
XX DT 25-MAR-2003 (updated)
XX DT 18-FEB-1991 (first entry)
XX DE Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
XX DE A protein encoded by pR123.
XX KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
XX KW plant toxin.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
XX FT Region 1..32
XX FT /note="Leader"
XX FT Region 33..302

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FT FT /note="A-chain"
FT FT 315..332
XX XX /note="B-chain"
XX PN EP237676-A.
XX PD 23-SEP-1987.
XX PF 13-NOV-1986; 86EP-0308877.
XX PR 07-MAR-1986; 86US-0837583.
XX PA (CETU ) CETUS CORP.
XX PA (CHIR ) CHIRON CORP.
XX PI Piatak M;
XX WPI; 1987-265177/38.
XX DR N-PSDB; AAN70519.
XX PT New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX PT by recombinant DNA procedures with specific isolation steps for
XX PS purer and soluble prods.
XX PS Disclosure; Fig 1; 112pp; English.
XX CC The full-length sequences encoding ricin A (AAN70520), ricin D
XX CC (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
XX CC form were obt'd. using messenger RNA to obtain a cDNA library, and
XX CC then probing the library to retrieve the desired cDNA inserts. The
XX CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
XX CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
XX CC plasmids contg. cDNA inserts obt'd. by probing a cDNA library for
XX CC sequences encoding ricin B using the probe in AAN70517. The cDNA
XX CC inserts can be placed into expression vectors. Site-directed
XX CC mutagenesis may be used to place an ATG start codon and a HindIII
XX CC site at the beginning of the mature protein (see AAN70518). The
XX CC coding sequences of the inserts can be ligated into expression
XX CC vectors contg. the PhOA promoter-operator and leader sequence
XX CC (AAN70523) and suitable retroregulators.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 332 AA;
    Query Match 99.5%; Score 1020; DB 8; Length 332;
    Best Local Similarity 100.0%; Pred. No. 3.6e-100;
    Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNVRGLPINQRFILV 61
Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNVRGLPINQRFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 121
Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFG 155
QY 122 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQIMISEAR 181
Db 156 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQIMISEAR 215
QY 182 FOYIEGEMTRIRYNRRS 199
Db 216 FOYIEGEMTRIRYNRRS 233
RESULT 7
AAP95639
ID AAP95639 standard; protein; 332 AA.
XX AC AAP95639;
XX DT 25-MAR-2003 (updated)
XX DT 31-OCT-2002 (updated)

```


DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 DE Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 XX Ricinus communis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..35
 FT /label= leader sequence
 FT Peptide 36..302
 FT /label=A-chain
 FT Peptide 303..314
 FT /label=linker
 FT Peptide 315..332
 FT /label=B-chain
 XX EP335476-A.
 XX 04-OCT-1989.
 XX 19-JAN-1989; 89EP-0201162.
 XX 08-FEB-1984; 84US-0578115.
 PR 08-FEB-1984; 84US-0578121.
 PR 09-FEB-1984; 84US-0578122.
 PR 07-SEP-1984; 84US-0648759.
 PR 20-SEP-1984; 84US-0653515.
 XX (CETU) CETUS CORPORATION.
 XX Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Placax NJ;
 XX WPI; 1989-286959/40.
 DR N-PSDB; AAN91281.
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 FT high cell specificity and good extracellular stability.
 XX Disclosure; Fig 14; 54pp; English.
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 332 AA;
 SQ Query Match 99.5%; Score 1020; DB 10; Length 332;
 Best Local Similarity 100.0%; Pred. No. 3.6e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFNTAGATVQSNTNFIRAVRGRUTTGADVREHEIPVLPNVRVGLPINORFILLV 61
 DB 36 IFPKQYPIINFNTAGATVQSNTNFIRAVRGRUTTGADVREHEIPVLPNVRVGLPINORFILLV 95
 QY 62 ELSNHAELSVTALDVNTAYVGVYRAGNSAYFFHPDNQDEAETHLFTDVQNRVTFAPG 121
 DB 96 ELSNHAELSVTALDVNTAYVGVYRAGNSAYFFHPDNQDEAETHLFTDVQNRVTFAPG 155
 QY 122 GNYDRLEQAGLNRENIELGNGLPEEATISALYYSTGGTQLPTLARSFCICQMISEAR 181
 DB 156 GNYDRLEQAGLNRENIELGNGLPEEATISALYYSTGGTQLPTLARSFCICQMISEAR 215

QY 182 FOYIEGEMTRIRYNRRS 199
 DB 216 FOYIEGEMTRIRYNRRS 233
 RESULT 8
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX AAR70827;
 AC 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX Anti-cataract immunotoxin.
 XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW PHB19; 4197X; monoclonal antibody; MAB.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..27
 FT /label= Sig_peptide
 FT /note= "phoA signal sequence"
 FT Domain 28..145
 FT /label= HEAVY
 FT /note= "MAB 4197X heavy chain"
 FT Peptide 148..166
 FT /label= LINKER
 FT Domain 169..274
 FT /label= LIGHT
 FT /note= "MAB 419X light chain"
 FT Domain 276..544
 FT /label= RICIN-A
 FT Peptide 549..554
 FT /label= TAG
 FT /note= "hexa-histidine tail"
 XX WO9503828-A1.
 XX 09-FEB-1995.
 XX 15-JUL-1994; 94WO-US07919.
 XX 02-AUG-1993; 93US-0101329.
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 FT extra:capsular cataract extraction.
 XX Disclosure; Fig.4; 68pp; English.
 XX The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium IgG3 MAB 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from PHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 554 AA;
 SQ Query Match 99.5%; Score 1020; DB 16; Length 554;
 Best Local Similarity 100.0%; Pred. No. 7.3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPLINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNRVGLPINQRFILV 61
 Db 278 IFPKQYPLINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNRVGLPINQRFILV 337
 QY 62 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 121
 Db 338 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 337
 QY 122 GNYDRLEQLAGNLENIELNGPLLEEAISALYYSTGGTQPLTLARSFFIICQMISEAAR 181
 Db 398 GNYDRLEQLAGNLENIELNGPLLEEAISALYYSTGGTQPLTLARSFFIICQMISEAAR 457
 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 458 FOYIEGEMTRIRYNRRS 475

RESULT 9
 AAP90079
 ID AAP90079 standard; protein; 562 AA.
 XX
 AC AAP90079;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE Ricin D.
 XX
 KW Ricin D; Ricinus communis; castor beans; Zanicbariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX
 OS Ricinus communis (castor beans).
 XX
 PN WO8904839-A.
 XX
 PD 01-JUN-1989.
 XX
 PF 23-NOV-1988; 88WO-US04238.
 XX
 PR 24-NOV-1987; 87US-0124735.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Brown EL, Jones S;
 XX
 DR WPI; 1989-178366/24.
 DR N-PSDB; AAN90068.
 XX
 PT Modified ricin molecules and toxin conjugates
 PT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 XX
 PS Disclosure; fig 1; 51pp; English.
 XX
 CC Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicbariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 562 AA;

Query Match 99.5%; Score 1020; DB 10; Length 562;
 Best Local Similarity 100.0%; Pred. No. 7.4e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPLINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNRVGLPINQRFILV 61
 Db 36 IFPKQYPLINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNRVGLPINQRFILV 95
 QY 62 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 121

Db 96 ELSNHAELS VTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 155
 QY 122 GNYDRLEQLAGNLENIELNGPLLEEAISALYYSTGGTQPLTLARSFFIICQMISEAAR 181
 Db 156 GNYDRLEQLAGNLENIELNGPLLEEAISALYYSTGGTQPLTLARSFFIICQMISEAAR 215
 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 216 FOYIEGEMTRIRYNRRS 233

RESULT 10
 AAG78304
 ID AAG78304 standard; Protein; 565 AA.
 XX
 AC AAG78304;
 XX
 DT 27-NOV-2001 (first entry)
 XX
 DE Modified castor bean preprorin (SEQ ID 10).
 XX
 KW Castor bean plant; preprorin; ricin; A chain; B chain;
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide; viral protease.
 XX
 OS Chimeric - Ricinus communis
 OS Chimeric - Human immunodeficiency virus type 2.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide
 FT 25..565
 FT /label= Prorin
 FT /note= "Prorin consists of the ricin A chain, a linker
 FT peptide, and the ricin B chain. Prorin is
 FT proteolytically cleaved between the A chain and
 FT the linker to yield mature ricin"
 FT
 FT Protein 25..291
 FT /label= Ricin_A_chain
 FT /note= "N-glycosidase"
 FT 292..303
 FT /label= Linker_peptide
 FT Cleavage-site 296..297
 FT /label= HIV_protease_cleavage_site
 FT 304..565
 FT /label= Ricin_B_chain
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
 XX
 PN WO200160393-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 15-FEB-2001; 2001WO-US05282.
 XX
 PR 16-FEB-2000; 2000US-0182759.
 XX
 PA (BECH-) BECHTEL BWXT IDAHO LLC.
 XX
 PI Keener WK, Ward TE;
 XX
 DR WPI; 2001-581908/65.
 DR N-PSDB; AAI64145.
 XX
 CC Novel composition comprising toxin e.g., ricin based antiviral compound
 CC useful for treating viral infections such as human immunodeficiency
 CC virus infection.
 XX
 PS Example 1; Page 59-63; 66pp; English.
 XX
 CC The sequence relates to the amino acid sequence of a modified preprorin
 CC protein encoded by AAI64145. The invention relates to a novel toxin
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected

CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
 CC virucide activities. The agent is able to enter all HIV susceptible
 CC cells, and not just cells known to act as host cells for the virus. The
 CC antiviral agent remains inert in a cell unless the cell is infected
 CC with the HIV virus, where the viral protease activates it. Ricin's
 CC mechanism of action is through inactivation of cellular ribosomes and
 CC enhancement of binding of the antiviral agent to galactose residues on
 CC cell surfaces, and its cellular internalisation. The invention is useful
 CC for treating human immunodeficiency virus infection and other viral
 CC infections, especially retroviral infections. The antiviral agent is
 CC activated in viral particles or early-stage infected cells, killing the
 CC cells upon infection and effectively preventing the integration of the
 CC viral genome into the host genome thereby preventing the latency/rebound
 CC problem.

XX Sequence 565 AA;
 SQ
 Query Match 99.5%; Score 1020; DB 22; Length 565;
 Best Local Similarity 100.0%; Pred. No. 7.5e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 84
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 121
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 144
 QY 122 GNYDRLEQLAGNLENIELGNGLPLEEALISALYYSTGGTQPLTLARSFIIQIMISEAR 181
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 145 GNYDRLEQLAGNLENIELGNGLPLEEALISALYYSTGGTQPLTLARSFIIQIMISEAR 204
 QY 182 FOYIEGEMRTRIRYNRRS 199
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 205 FOYIEGEMRTRIRYNRRS 222

RESULT 11

AAP70326

ID AAP70326 standard; Protein; 576 AA.

XX AAP70326;

XX AC

XX 25-MAR-2003 (updated)

DT 21-MAY-1991 (first entry)

XX Sequence of Ricinus communis (castor bean) Ricin toxin
 DE (RT or ricin) E precursor encoded by pRT38.
 DE

XX Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
 KW plant toxin.
 KW

XX Ricinus communis.

XX OS

XX Key Location/Qualifiers

XX Region 1..35

FT /note= "leader"

FT Region 36..302

FT /note= "A-chain"

FT Region 315..576

FT /note= "B-chain"

XX EP237676-A.

XX 23-SEP-1987.

XX 13-NOV-1986; 86EP-0308877.

XX 07-MAR-1986; 86US-0837583.

XX (CETU) CETUS CORP.

XX (CHIR) CHIRON CORP.

PA

XX Piatak M;

PI

XX WPI; 1987-265177/38.

XX N-PSDB; AAN70526.

XX New non-glycosylated ricin precursor and toxin etc. - are prepd.
 FT by recombinant DNA procedures with specific isolation steps for
 FT purer and soluble prods.

XX Disclosure; Fig 14(1-2); 112pp; English.

XX The full length sequences encoding ricin A (AAN70520), ricin D

CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor

CC form were obtained, using the messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see

CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three

CC plasmids containing cDNA inserts obtained by probing a cDNA library

CC for sequences encoding ricin B using the probe in AAN70517. The cDNA

CC inserts can be placed into expression vectors. Site-directed

CC mutagenesis may be used to place an ATG start codon and a HindIII

CC site at the beginning of the mature protein, (see AAN70518). The

CC coding sequences of the inserts can be ligated into expression

CC vectors containing the Phox promoter-operator and leader sequence

CC (AAN70523) and suitable retroregulators.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 576 AA;

SQ

Query Match 99.5%; Score 1020; DB 8; Length 576;

Best Local Similarity 100.0%; Pred. No. 7.7e-100;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

36 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 121

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 155

QY 122 GNYDRLEQLAGNLENIELGNGLPLEEALISALYYSTGGTQPLTLARSFIIQIMISEAR 181

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

156 GNYDRLEQLAGNLENIELGNGLPLEEALISALYYSTGGTQPLTLARSFIIQIMISEAR 215

QY 182 FOYIEGEMRTRIRYNRRS 199

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

216 FOYIEGEMRTRIRYNRRS 233

XX

RESULT 12

AAW25787

ID AAW25787 standard; Protein; 576 AA.

XX AAW25787;

XX AC

XX 25-MAR-2003 (updated)

DT 27-MAR-1998 (first entry)

XX Castorbean ricin.

XX

XX Ricin; cytotoxin; hybrid protein; cell delivery;

KW cell binding ligand; translocation domain; diphtheria toxin B';

KW interleukin-2; T-cell lymphoma; organ rejection; therapy.

XX Ricinus communis.

XX OS

XX Key Location/Qualifiers

XX Peptide 1..35

FT /label= Sig_peptide

FT Protein 36..302

FT /label= A-domain

FT FT

Peptide 303...314
/label= Linker
Domain 315...576
/label= B-domain

US5668255-A.

16-SEP-1997.

04-AUG-1993; 93US-0102387.

27-JUN-1991; 91US-0722484.

27-JUN-1984; 84US-0618199.

25-APR-1985; 85US-0726808.

27-JUN-1985; 85US-0742554.

22-DEC-1989; 89US-0456095.

14-JUN-1990; 90US-0538276.

04-AUG-1993; 93US-0102387.

(SERA-) SERAGEN INC.

Murphy JR;

WPI; 1997-470103/43.

N-PSDB; AAT91638.

New hybrid molecules for delivery of agents to cells - comprise a

binding domain of a cell binding ligand and a portion of a

translocation domain of a protein

Example 4; Fig 11A-B; 30pp; English.

This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see AAY5892) encoding the enzymatic A domain and a portion

of the A-to-B linker peptide of ricin was used to construct a

ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in

E. coli. The hybrid protein can be isolated and used to treat

conditions involving over-production of cells bearing IL2 receptors,

such as certain T-cell lymphomas and organ transplant rejection

crises. The hybrid inactivates ribosomes in cells bearing IL2

receptors, resulting in cessation of protein synthesis and death of

target cells. Claimed hybrid proteins comprise a translocation

domain and a cell binding domain from e.g. a hormone, growth factor

or polypeptide toxin. The hybrid molecules can be used for the

delivery of agents (e.g. therapeutic genes, toxins, detectable

labels) into cells. The use of a translocation mechanism ensures

that the hybrid will be effective in relatively low doses, since a

high proportion of the substance of interest will be taken into the

targeted cells. The hybrid molecules can be manufactured as a

single hybrid recombinant protein, permitting reproducibility,

consistency, and the precise control of composition.

(Updated on 25-MAR-2003 to correct PF field.)

PT Peptide 303...314
FT /label= Linker
FT Domain 315...576
FT /label= B-domain
XX US5668255-A.
XX 16-SEP-1997.
XX 04-AUG-1993; 93US-0102387.
XX 27-JUN-1991; 91US-0722484.
XX 27-JUN-1984; 84US-0618199.
XX 25-APR-1985; 85US-0726808.
XX 27-JUN-1985; 85US-0742554.
XX 22-DEC-1989; 89US-0456095.
XX 14-JUN-1990; 90US-0538276.
XX 04-AUG-1993; 93US-0102387.
XX (SERA-) SERAGEN INC.
XX Murphy JR;
XX WPI; 1997-470103/43.
XX N-PSDB; AAT91638.
XX New hybrid molecules for delivery of agents to cells - comprise a
XX binding domain of a cell binding ligand and a portion of a
XX translocation domain of a protein
XX Example 4; Fig 11A-B; 30pp; English.
XX This polypeptide comprises the castorbean cytotoxin, ricin.
XX DNA (see AAY5892) encoding the enzymatic A domain and a portion
XX of the A-to-B linker peptide of ricin was used to construct a
XX ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in
XX E. coli. The hybrid protein can be isolated and used to treat
XX conditions involving over-production of cells bearing IL2 receptors,
XX such as certain T-cell lymphomas and organ transplant rejection
XX crises. The hybrid inactivates ribosomes in cells bearing IL2
XX receptors, resulting in cessation of protein synthesis and death of
XX target cells. Claimed hybrid proteins comprise a translocation
XX domain and a cell binding domain from e.g. a hormone, growth factor
XX or polypeptide toxin. The hybrid molecules can be used for the
XX delivery of agents (e.g. therapeutic genes, toxins, detectable
XX labels) into cells. The use of a translocation mechanism ensures
XX that the hybrid will be effective in relatively low doses, since a
XX high proportion of the substance of interest will be taken into the
XX targeted cells. The hybrid molecules can be manufactured as a
XX single hybrid recombinant protein, permitting reproducibility,
XX consistency, and the precise control of composition.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 576 AA;
SQ Query Match 99.5%; Score 1020; DB 18; Length 576;
Best Local Similarity 100.0%; Pred. No. 7-7e-100;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNKGPIINQRFILV 61
Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNKGPIINQRFILV 95
QY 62 ELSNHAELSVTLADVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQRYTFAFG 121
Db 96 ELSNHAELSVTLADVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQRYTFAFG 155
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALYYSTGTGTLPTLARSFIICQMISEAR 181
Db 156 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALYYSTGTGTLPTLARSFIICQMISEAR 215
QY 182 FOYIEGEMTRIRYNRRS 199
|||||

Db 216 FOYIEGEMTRIRYNRRS 233

RESULT 13

AAY5892

ID AAY5892 standard; Protein; 576 AA.

XX AC AAY5892;

XX DT 15-FEB-2000 (first entry)

XX DE Castor bean ricin toxin.

XX KW Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria;
XX KW translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus;
XX KW shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV;
XX KW cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison;
XX KW adipocyte; cancer; virus; infection; antibody.

XX OS Ricinus communis.

XX PN US5965406-A.

XX PD 12-OCT-1999.

XX PF 07-JUN-1995; 95US-0488246.

XX PR 04-AUG-1993; 93US-0102387.

XX PR 07-JUN-1984; 84US-0618199.

XX PR 27-JUN-1991; 91US-0722484.

XX PR 25-APR-1985; 85US-0726808.

XX PR 07-JUN-1985; 85US-0742554.

XX PR 22-DEC-1989; 89US-0456095.

XX PR 14-JUN-1990; 90US-0538276.

XX (SERA-) SERAGEN INC.

XX PI Murphy JR;

XX WPI; 1999-632431/54.

XX N-PSDB; AAZ30663.

Recombinant DNA molecule encoding a three part hybrid protein used in

the treatment of Aids and genetic deficiency diseases -

Example 4; Fig 11; 31pp; English.

The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the Castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells.

XX Sequence 576 AA;

Query Match 99.5%; Score 1020; DB 20; Length 576;
 Best Local Similarity 100.0%; Pred. No. 7.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPNRVGLPINORFILV 61
 DB 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPNRVGLPINORFILV 95
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 121
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 155
 QY 122 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQPLTLARSFIIQIMISEAR 181
 DB 156 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQPLTLARSFIIQIMISEAR 215
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 14
 AAY78592
 ID AAY78592 standard; Protein; 576 AA.
 AC AAY78592;
 XX

DT 05-MAY-2000 (first entry)
 DE Ricinus communis ricin protein sequence.

KW Ricin; toxin; hybrid protein; translocation domain; cell destruction;
 KW cell binding domain; Genetic deficiency disease; cell targeting; cancer;
 KW adipocyte; enzyme delivery; anti-viral; HIV.

OS Ricinus communis.

PN US6022950-A.

PD 08-FEB-2000.

PF 07-JUN-1995; 95US-0479510.

PR 07-JUN-1984; 84US-0618199.

PR 27-JUN-1991; 91US-0722484.

PR 25-APR-1985; 85US-0726808.

PR 07-JUN-1985; 85US-0742554.

PR 22-DEC-1989; 89US-0456095.

PR 14-JUN-1990; 90US-0538276.

PR 04-AUG-1993; 93US-0102387.

PA (SERA-) SERAGEN INC.

PI Murphy JR;

XX WPI: 2000-160390/14.

DR N-PSDB; AA290019.

XX New two-part hybrid protein comprising a translocation domain and a
 PT cell-binding domain, for treating genetic deficiency diseases, cancer
 PT and HIV infections -

PS Example 4; Fig 11; 32pp; English.

XX This sequence represents the Ricinus communis ricin protein sequence. The
 CC toxin can be included in the hybrid protein of the invention and used to
 CC destroy or modify the cell that the hybrid protein is targeted to. The
 CC hybrid protein comprises a first part which is a portion of the binding
 CC domain of a cell-binding ligand, effective to cause the hybrid molecule
 CC to bind to a cell of an animal. The second part comprises a portion of a
 CC translocation domain of a naturally occurring protein (e.g. the
 CC translocation domain of diphtheria toxin) the second part translocates
 CC the third part across the cytoplasmic membrane and into the cytosol of

CC the cell. The third part comprises a chemical entity to be introduced
 CC into the cell, where each of the first and third part is non-native with
 CC respect to naturally occurring protein, and the covalent bond attaching
 CC the second and third part is cleavable. The toxin represented by the
 CC present sequence can form part of the third portion of the hybrid
 CC protein. The cell binding domain binds to a specific cell and the
 CC translocation domain transfers the hybrid molecule across the cell
 CC membrane into the cytosol. The third part of the protein, linked to its
 CC translocation domain through a cleavable bond, can then carry out its
 CC function. The hybrid molecules are useful for treating genetic deficiency
 CC diseases by delivering to affected cells an enzyme supplying the missing
 CC function, to supplement cellular levels of a particular enzyme or a
 CC scarce precursor or cofactor, to direct toxins or other poisons to
 CC destroy particular cells (such as adipocytes, cancer cells, or
 CC virus-infected cells), and to counteract viral infections such as HIV by
 CC introducing into appropriate cells antibodies to viral proteins.

XX Sequence 576 AA;

Query Match 99.5%; Score 1020; DB 21; Length 576;
 Best Local Similarity 100.0%; Pred. No. 7.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPNRVGLPINORFILV 61

DB 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPNRVGLPINORFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 121

DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQPLTLARSFIIQIMISEAR 181

DB 156 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQPLTLARSFIIQIMISEAR 215

QY 182 FOYIEGEMTRIRYNRRS 199

DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 15

AAG78301

ID AAG78301 standard; Protein; 576 AA.

AC AAG78301;

DT 15-NOV-2001 (first entry)

DE Castor bean prepropricin protein (SEQ ID 2).

XX Castor bean plant; prepropricin; ricin; A chain; B chain;

XX human immunodeficiency virus infection; HIV; toxin; antiviral agent;

XX retroviral infection; anti-HIV; virucide activity; viral protease.

OS Ricinus communis.

XX Key Location/Qualifiers

FT Peptide 1..35

FT /label= Signal peptide

FT Protein 36..302

FT /label= Ricin_A_chain

FT /note= "N-glycosidase"

FT Peptide 303..314

FT /label= Linker peptide

FT /note= "Cleaved during activation of ricin"

FT Protein 315..576

FT /label= Ricin_B_chain

XX /note= "Galactose/N-acetylgalactosamine-binding lectin"

PN WO200160393-A1.

XX 23-AUG-2001.

XX

PF 15-FEB-2001; 2001WO-US05282.
XX
PR 16-FEB-2000; 2000US-0182759.
XX
PA (BECH-) BECHTEL BWXT IDAHO LLC.
XX
PI Keener WK, Ward TE;
XX
DR WPI; 2001-581908/65.
DR N-ESDB; AAI64138.
XX
XX
PT Novel composition comprising toxin e.g., ricin based antiviral compound
PT useful for treating viral infections such as human immunodeficiency
PT virus infection.
XX
XX Disclosure; Page 50-54; 66pp; English.
XX
XX The sequence relates to prepropricin protein encoded by the DNA sequence
CC given in AAI64138. The invention relates to a novel toxin (e.g., ricin)
CC based antiviral agent which is toxic to virus-infected cells, but
CC non-toxic to uninfected cells. The invention has anti-HIV and virucide
CC activities. Its mechanism of action is through inactivation of cellular
CC ribosomes and enhancement of binding of the antiviral agent to galactose
CC residues on cell surfaces, and its cellular internalisation. The
CC invention is useful for treating human immunodeficiency virus infection
CC and other viral infections, especially retroviral infections. The
CC antiviral agent is activated in viral particles or early-stage infected
CC cells, killing the cells upon infection and effectively preventing the
CC integration of the viral genome into the host genome thereby preventing
CC the latency/rebound problem. The agent enters all HIV susceptible cells,
CC and not just cells known to act as host cells for the virus. The
CC antiviral agent remains inert in a cell until degraded in it, unless the
CC cell is infected with the virus, where the viral protease activates it.
XX
SQ Sequence 576 AA;

Query Match 99.5%; Score 1020; DB 22; Length 576;
Best Local Similarity 100.0%; Pred. No. 7.7e-100;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILV 61
Db |||||
36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILV 95
Qy 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTTFAG 121
Db |||||
96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTTFAG 155
Qy 122 GNYDRLEQLAGNRENIELGNGLPLEEALSALYYSTGQTLPILARSFIIQIMISEAAR 181
Db |||||
156 GNYDRLEQLAGNRENIELGNGLPLEEALSALYYSTGQTLPILARSFIIQIMISEAAR 215
Qy 182 FQYIEGEMRIRYNRRS 199
Db |||||
216 FQYIEGEMRIRYNRRS 233

Search completed: February 10, 2004, 16:22:26
Job time : 34.9288 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 11.5063 Seconds
(without alignments)
731.761 Million cell updates/sec

Title: US-10-083-336A-5

Perfect score: 1025

Sequence: 1 MIFPKQPIINFTAGATVQ.....ARFQIEGEMTRIRYNRRS 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap:*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap:*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pap:*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap:*

5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pap:*

6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025	100.0	268	2	US-08-356-786-8
2	1025	100.0	534	2	US-08-356-786-10
3	1020	99.5	267	1	US-07-901-707-1
4	1020	99.5	267	1	US-07-988-430-1
5	1020	99.5	267	1	US-08-425-336-1
6	1020	99.5	267	1	US-08-488-113B-1
7	1020	99.5	267	1	US-08-477-484B-1
8	1020	99.5	267	2	US-08-646-360-1
9	1020	99.5	267	3	US-08-839-765-1
10	1020	99.5	267	3	US-09-136-389-1
11	1020	99.5	267	4	US-09-610-838-1
12	1020	99.5	267	5	PCT-US92-09487-1
13	1020	99.5	290	1	US-08-378-761A-27
14	1020	99.5	290	1	US-08-485-286-27
15	1020	99.5	290	6	US-08-485-286-27
16	1010	98.5	267	1	US-08-218-303-16
17	1010	98.5	267	2	US-08-338-793D-61
18	1010	98.5	267	4	US-09-538-873-1
19	930.5	90.8	540	1	US-08-378-761A-77
20	930.5	90.8	540	1	US-08-485-286-77
21	342	33.4	247	1	US-08-488-113B-6
22	342	33.4	247	1	US-08-477-484B-6
23	342	33.4	247	2	US-08-646-360-6
24	342	33.4	247	3	US-08-839-765-6
25	342	33.4	247	3	US-09-136-389-6
26	342	33.4	247	4	US-09-610-838-6
27	342	33.4	267	1	US-08-378-761A-74

28	342	33.4	267	1	US-08-485-286-74	Sequence 74, Appl
29	342	33.4	289	1	US-07-923-692C-4	Sequence 4, Appl
30	342	33.4	289	1	US-08-184-237-4	Sequence 4, Appl
31	342	33.4	289	2	US-08-482-920-4	Sequence 4, Appl
32	342	33.4	289	3	US-08-484-341-4	Sequence 4, Appl
33	342	33.4	289	3	US-08-483-502-4	Sequence 4, Appl
34	342	33.4	289	4	US-09-726-651A-4	Sequence 4, Appl
35	341.5	32.3	282	1	US-08-324-301-15	Sequence 15, Appl
36	329.5	32.1	250	1	US-08-378-761A-71	Sequence 71, Appl
37	329.5	32.1	250	1	US-08-485-286-71	Sequence 71, Appl
38	323.5	31.6	251	4	US-09-538-873-3	Sequence 3, Appl
39	312.5	30.5	255	1	US-07-901-707-6	Sequence 6, Appl
40	312.5	30.5	255	1	US-07-988-430-6	Sequence 6, Appl
41	312.5	30.5	255	1	US-08-425-336-6	Sequence 6, Appl
42	312.5	30.5	255	5	PCT-US92-09487-6	Sequence 6, Appl
43	312	30.4	248	3	US-08-902-486-7	Sequence 7, Appl
44	312	30.4	290	1	US-08-245-754A-2	Sequence 2, Appl
45	312	30.4	290	2	US-08-597-731-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305

GENERAL INFORMATION:

APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: King, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/831,967

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-053

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-356-786-8

Query Match 100.0%; Score 1025; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 GNYDRLEQAGNLTENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 4

US-07-988-430-1
 ; Sequence 1, Application US/07988430
 ; Patent No. 5416202
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernhard, Susan L.
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Lane, Julie A.
 ; APPLICANT: Lei, Shau-Ping
 ; TITLE OF INVENTION: Materials Comprising and Methods of
 ; Preparation and Use for Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; STREET: Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/988,430
 ; FILING DATE: 19921209
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5416202and, Greta E.
 ; REGISTRATION NUMBER: 35302
 ; REFERENCE/DOCKET NUMBER: 31133
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-988-430-1

Query Match 99.5%; Score 1020; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Mismatches 0; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 122 GNYDRLEQAGNLTENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 181
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 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 5

US-08-425-336-1
 ; Sequence 1, Application US/08425336
 ; Patent No. 5621083
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 140
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/425,336
 ; FILING DATE: 18-APR-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Thomas C.
 ; REGISTRATION NUMBER: P-36,989
 ; REFERENCE/DOCKET NUMBER: 31394
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-425-336-1

Query Match 99.5%; Score 1020; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Mismatches 0; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHETPVLNPRVGLPINQRFILV 61
 Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHETPVLNPRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAPG 121
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAPG 120
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Best Local Similarity 100.0%; Pred. No. 2.3e-111; Mismatches 0; Gaps 0;
Matches 198; Conservative 0; Indels 0; Gaps 0;

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Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVHRHEIPVLPNVRVGLPINORFILV 60

QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDQVQRYTFAPG 121
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDQVQRYTFAPG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 8
US-08-646-360-1
; Sequence 1, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8989
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-1

Query Match 99.5%; Score 1020; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVHRHEIPVLPNVRVGLPINORFILV 61
Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVHRHEIPVLPNVRVGLPINORFILV 60

QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDQVQRYTFAPG 121
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDQVQRYTFAPG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-839-765-1

Query Match 99.5%; Score 1020; DB 3; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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 QY 122 GNYDRLEQLAGNLEINELGNPLEEASALYYSTGCTQLPTLARSFIIICIQMISEAAR 181
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 QY 182 FOYIEGEMRTRIRYNRS 199
 DB 181 FOYIEGEMRTRIRYNRS 198

RESULT 10

US-09-136-389-1
 Sequence 1, Application US/09136389
 Patent No. 6146850

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,389
 FILING DATE: 12-MAY-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-136-389-1

Query Match 99.5%; Score 1020; DB 3; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61
 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
 DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
 QY 122 GNYDRLEQLAGNLEINELGNPLEEASALYYSTGCTQLPTLARSFIIICIQMISEAAR 181
 DB 121 GNYDRLEQLAGNLEINELGNPLEEASALYYSTGCTQLPTLARSFIIICIQMISEAAR 180
 QY 182 FOYIEGEMRTRIRYNRS 199
 DB 181 FOYIEGEMRTRIRYNRS 198

RESULT 11

US-09-610-838-1
 Sequence 1, Application US/09610838
 Patent No. 6376217

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/610,838
 FILING DATE: 06-JUL-2000
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,389
 FILING DATE: 18-AUG-1998
 APPLICATION NUMBER: 08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348

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; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-1

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Query Match      99.5%; Score 1020; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 1PPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60

QY      62 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
Db      61 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120

QY      122 GNYDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 181
Db      121 GNYDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 180

QY      182 FOYIEGEMRTRIRYNRRS 199
Db      181 FOYIEGEMRTRIRYNRRS 198

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RESULT 12
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1

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Query Match      99.5%; Score 1020; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      62 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
Db      61 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120

QY      122 GNYDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 181
Db      121 GNYDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 180

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Db      181 FOYIEGEMRTRIRYNRRS 198

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RESULT 13
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,761A
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 290 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-378-761A-27

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Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 122 GNYDRLEQLAGNRENIELGNGLPLEEASALYYSTGGTQTLPLARSFIICQMISEAAR 181
DB 145 GNYDRLEQLAGNRENIELGNGLPLEEASALYYSTGGTQTLPLARSFIICQMISEAAR 204

QY 182 FOYIEGEMTRIRYNRRS 199
DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 14
US-08-485-286-27
;; Sequence 27, Application US/08485286
;; Patent No. 5646026
;; Patent No. 5646026 5646119
;; GENERAL INFORMATION:
;; APPLICANT: WALSH, TERENCE A
;; APPLICANT: HEY, TIMOTHY D
;; APPLICANT: MORGAN, ALICE ER
;; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;; TITLE OF INVENTION: USING
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ANDREA T. BORUCKI
;; STREET: 9330 ZIONSVILLE ROAD
;; CITY: INDIANAPOLIS
;; STATE: IN
;; COUNTRY: US
;; ZIP: 46268
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/485,286
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/378761
;; FILING DATE: 26-JAN-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 290 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-485-286-27

Query Match 99.5%; Score 1020; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNRVGLPINQRIILV 84

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 121
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DB 145 GNYDRLEQLAGNRENIELGNGLPLEEASALYYSTGGTQTLPLARSFIICQMISEAAR 204

QY 182 FOYIEGEMTRIRYNRRS 199
DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 15
5248606-4
;; Patent No. 5248606
;; APPLICANT: WALSH, TERENCE A; HEY, TIMOTHY D; MORGAN,
;; ALICE E.R.
;; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
;; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATION
;; NUMBER OF SEQUENCES: 49
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/535,636
;; FILING DATE: 11-JUN-1990
;; SEQ ID NO: 4
;; LENGTH: 290
5248606-4

Query Match 99.5%; Score 1020; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 182 FOYIEGEMTRIRYNRRS 199
DB 205 FOYIEGEMTRIRYNRRS 222

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Sun Feb 15 07:29:58 2004

us-10-083-336a-5.rai

Page 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-5

Perfect score: 1025

Sequence: 1 MIFPKQYPIINFTTAGATVQ.....ARFQIEGEMTRIRNRRS 199

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Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1020	99.5	198	12	US-10-083-336A-3
4	1020	99.5	267	12	US-10-127-890-1
5	1020	99.5	576	12	US-10-083-336A-1
6	1010	98.5	198	12	US-10-083-336A-7
7	1010	98.5	267	12	US-10-282-935-1
8	1010	98.5	267	12	US-10-440-796-1
9	956	93.3	189	12	US-10-083-336A-6
10	956	93.3	190	12	US-10-083-336A-11
11	951	92.8	188	12	US-10-083-336A-4
12	941	91.8	188	12	US-10-083-336A-8
13	934.5	91.2	185	12	US-10-083-336A-9
14	748	73.0	179	12	US-10-083-336A-2
15	342	33.4	247	10	US-09-792-793A-39

16	342	33.4	247	12	US-10-127-890-6	Sequence 6, Appli
17	342	33.4	247	12	US-10-375-209A-39	Sequence 39, Appli
18	342	33.4	289	12	US-10-280-679B-4	Sequence 4, Appli
19	323.5	31.6	251	12	US-10-282-935-3	Sequence 3, Appli
20	323.5	31.6	251	12	US-10-440-796-3	Sequence 3, Appli
21	312	30.4	247	10	US-09-792-793A-34	Sequence 34, Appli
22	312	30.4	247	12	US-10-375-209A-34	Sequence 34, Appli
23	279	27.2	263	12	US-10-127-890-4	Sequence 4, Appli
24	277	27.0	263	12	US-10-127-890-7	Sequence 7, Appli
25	276	26.9	252	9	US-09-347-064-2	Sequence 2, Appli
26	276	26.9	252	9	US-09-347-064-8	Sequence 8, Appli
27	267.5	26.1	248	12	US-10-127-890-5	Sequence 5, Appli
28	246.5	24.0	251	12	US-10-127-890-110	Sequence 110, App
29	246.5	24.0	251	12	US-10-127-890-111	Sequence 111, App
30	245.5	24.0	251	12	US-10-127-890-101	Sequence 101, App
31	244.5	23.9	251	12	US-10-127-890-99	Sequence 99, Appl
32	244.5	23.9	251	12	US-10-127-890-107	Sequence 107, App
33	243.5	23.8	251	12	US-10-127-890-100	Sequence 100, App
34	243.5	23.8	251	12	US-10-127-890-106	Sequence 106, App
35	242.5	23.7	251	9	US-09-765-527-247	Sequence 247, App
36	242.5	23.7	251	12	US-10-127-890-2	Sequence 2, Appli
37	242.5	23.7	251	12	US-10-127-890-102	Sequence 102, App
38	242.5	23.7	251	12	US-10-127-890-103	Sequence 103, App
39	242.5	23.7	251	12	US-10-127-890-104	Sequence 104, App
40	242.5	23.7	251	12	US-10-127-890-105	Sequence 105, App
41	242.5	23.7	316	12	US-10-074-596-1	Sequence 1, Appli
42	242.5	23.7	507	12	US-10-074-596-11	Sequence 11, Appl
43	241.5	23.6	251	12	US-10-127-890-109	Sequence 109, App
44	241.5	23.6	293	9	US-09-765-527-259	Sequence 259, App
45	241.5	23.6	309	9	US-09-765-527-253	Sequence 253, App

ALIGNMENTS

RESULT 1

US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-5

Query Match	100.0%	Score	1025;	DB	12;	Length	199;
Best Local Similarity	100.0%	Pred. No.	1.5e-109;				
Matches	199;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRIEIPVLPNRVGLPINORFTL	60				
Db	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRIEIPVLPNRVGLPINORFTL	60				
QY	61	VELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNYTFAF	120				
Db	61	VELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNYTFAF	120				
QY	121	GGNYDRLEQAGNLENIELGNGLPBLEEAIISALYYSTGTQTLPTLARSFIICMISEAA	180				
Db	121	GGNYDRLEQAGNLENIELGNGLPBLEEAIISALYYSTGTQTLPTLARSFIICMISEAA	180				
QY	181	RFQYIEGEMTRIRNRRS	199				


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Db 181 RFQIEGEMTRIRYNRS 199
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RESULT 2
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10
Query Match 100.0%; Score 1025; DB 12; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.5e-109; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;
Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAHEIPVLPNVRGLPINQRFILV 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAHEIPVLPNVRGLPINQRFILV 60
Qy 61 VELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYYTFAP 120
Db 61 VELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYYTFAP 120
Qy 121 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYVYSTGGTOLPTLARSFFIICOMISEAA 180
Db 121 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYVYSTGGTOLPTLARSFFIICOMISEAA 180
Qy 181 RFQIEGEMTRIRYNRS 199
Db 181 RFQIEGEMTRIRYNRS 199
RESULT 3
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3
Query Match 99.5%; Score 1020; DB 12; Length 198;
Best Local Similarity 100.0%; Pred. No. 5.5e-109; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 0;
Qy 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAHEIPVLPNVRGLPINQRFILV 61
|||||
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAHEIPVLPNVRGLPINQRFILV 60
62 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYYTFAPG 121
61 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYYTFAPG 120
122 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYVYSTGGTOLPTLARSFFIICOMISEAA 181
121 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYVYSTGGTOLPTLARSFFIICOMISEAA 180
182 FOYIEGEMTRIRYNRS 199
181 FOYIEGEMTRIRYNRS 198
RESULT 4
US-10-127-890-1
; Sequence 1, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
Query Match 99.5%; Score 1020; DB 12; Length 267;
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Best Local Similarity 100.0%; Pred. No. 8.5e-109; Mismatches 0; Indels 0; Gaps 0;
Matches 198; Conservative 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
DB 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 120
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 181
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 180
QY 182 FOYIEGEMRTRIRYNRRS 199
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 5
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match 99.5%; Score 1020; DB 12; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
DB 36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 155
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 181
DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 215
QY 182 FOYIEGEMRTRIRYNRRS 199
DB 216 FOYIEGEMRTRIRYNRRS 233

RESULT 6
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
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; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match 98.5%; Score 1010; DB 12; Length 198;
Best Local Similarity 100.0%; Pred. No. 7.8e-108;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 63
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 62
QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 123
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 122
QY 124 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 183
DB 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 182
QY 184 YIEGEMRTRIRYNRRS 199
DB 183 YIEGEMRTRIRYNRRS 198

RESULT 7
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: US/10/282,935
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/125,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-282-935-1

Query Match 98.5%; Score 1010; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 63
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 62
QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 123
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 122
QY 124 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 183
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|||||
Db 123 YDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 182
|||||
Qy 184 YIEGEMTRIRYNRRS 199
|||||
Db 183 YIEGEMTRIRYNRRS 198
|||||

RESULT 8
US-10-440-796-1
; Sequence 1, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/10/440,796
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2003-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-440-796-1

Query Match 98.5%; Score 1010; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-107; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0;

Qy 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 63
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
Qy 64 SNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123
Db 63 SNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
Qy 124 YDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 183
Db 123 YDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 182
Qy 184 YIEGEMTRIRYNRRS 199
Db 183 YIEGEMTRIRYNRRS 198

RESULT 9
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match 93.3%; Score 956; DB 12; Length 189;
Best Local Similarity 95.0%; Pred. No. 1.2e-101; Indels 10; Gaps 1;
Matches 189; Conservative 0; Mismatches 0;

Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFIL 50
Qy 61 VELSNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAF 120
Db 51 VELSNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAF 110
Qy 121 GGNVDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 180
Db 111 GGNVDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 170
Qy 181 RFQYIEGEMTRIRYNRRS 199
Db 171 RFQYIEGEMTRIRYNRRS 189

RESULT 10
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match 93.3%; Score 956; DB 12; Length 190;
Best Local Similarity 95.0%; Pred. No. 1.2e-101; Indels 10; Gaps 1;
Matches 189; Conservative 0; Mismatches 0;

Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFIL 50
Qy 61 VELSNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAF 120
Db 51 VELSNHAEISVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAF 110
Qy 121 GGNVDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 180
Db 111 GGNVDRLEQAGNRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 170
Qy 181 RFQYIEGEMTRIRYNRRS 199
Db 171 RFQYIEGEMTRIRYNRRS 189

RESULT 11
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
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; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match          92.8%; Score 951; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 4.5e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY  2  IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNVRGLPINQRFILV 61
Db  1  IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLT-----VLPNVRGLPINQRFILV 50
QY  62  ELSNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db  51  ELSNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110
QY  122  GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 181
Db  111  GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAR 170
QY  182  FOYIEGEMTRIRYNRRS 199
Db  171  FOYIEGEMTRIRYNRRS 188

RESULT 12
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match          91.8%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 6.3e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY  4  PKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNVRGLPINQRFILVEL 63
Db  3  PKQYPIINFNTAGATVQSYTNFIRAVRGRLT-----VLPNVRGLPINQRFILVEL 52
QY  64  SNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123
Db  53  SNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
QY  124  YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAARFQ 183

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Db  113  YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAARFQ 172
QY  184  YIEGEMTRIRYNRRS 199
Db  173  YIEGEMTRIRYNRRS 188

RESULT 13
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match          91.2%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.5e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY  2  IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNVRGLPINQRFILV 61
Db  1  IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
QY  62  ELSNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db  48  ELSNHAELSVTLALDVNTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 107
QY  122  GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 181
Db  108  GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 167
QY  182  FOYIEGEMTRIRYNRRS 199
Db  168  FOYIEGEMTRIRYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match          73.0%; Score 748; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 9.4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 10, 2004, 16:53:52
Job time : 31.6679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: . February 10, 2004, 16:18:30 ; Search time 10.8703 Seconds
(without alignments)
731.761 Million cell updates/sec

Title: US-10-083-336A-8
Perfect score: 965
Sequence: 1 MYPQYPIINFTTAGNVQS.....ARFOYTEGEMTRIRYNRRS 188

Scoring table: BLOSUM62

Searched: 328717 seqs. 42310858 residues

Total number of hits satisfying chosen parameters: 328717

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45

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Issued Patents AA:*
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3: /cgm2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgm2_6/ptodata/1/iaa/6B COMB pep.*
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6: /cgm2_6/ptodata/1/iaa/backfiles1.pe

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	950	98.4	267	1	Sequence 16, Appl
2	950	98.4	267	2	Sequence 61, Appl
3	950	98.4	267	4	Sequence 1, Appl
4	941	97.5	267	1	Sequence 1, Appl
5	941	97.5	267	1	Sequence 1, Appl
6	941	97.5	267	1	Sequence 1, Appl
7	941	97.5	267	1	Sequence 1, Appl
8	941	97.5	267	1	Sequence 1, Appl
9	941	97.5	267	2	Sequence 1, Appl
10	941	97.5	267	3	Sequence 1, Appl
11	941	97.5	267	3	Sequence 1, Appl
12	941	97.5	267	4	Sequence 1, Appl
13	941	97.5	267	5	Sequence 1, Appl
14	941	97.5	268	2	Sequence 8, Appl
15	941	97.5	290	1	Sequence 27, Appl
16	941	97.5	290	1	Sequence 27, Appl
17	941	97.5	290	6	Sequence 27, Appl
18	941	97.5	534	2	Patent No. 5248606-4
19	851.5	88.2	540	2	Sequence 10, Appl
20	851.5	88.2	540	1	Sequence 77, Appl
21	336	34.8	247	1	Sequence 77, Appl
22	336	34.8	247	1	Sequence 6, Appl
23	336	34.8	247	2	Sequence 6, Appl
24	336	34.8	247	3	Sequence 6, Appl
25	336	34.8	247	3	Sequence 6, Appl
26	336	34.8	247	4	Sequence 6, Appl
27	336	34.8	267	1	Sequence 74, Appl

Query Match 98.4%: Score 950: DB 1: Length 267:

Best Local Similarity	94.9%	Pred. No. 1.2e-102;	0; Mismatches 0;	Indels 10; Gaps 1;
Matches 188;	Conservative			

0V 1 MVPKOYPIINFTTAGATVOSYTNFIRAVRGRLT-----VLPNRVGLPINORFILV 50

Sequence 74	Appli
Sequence 4	Appli
Sequence 4	Appli
Sequence 4	Appli
Sequence 4	Appli
Sequence 4	Appli
Sequence 4	Appli
Sequence 15	Appli
Sequence 6	Appli
Sequence 6	Appli
Sequence 6	Appli
Sequence 7	Appli
Sequence 2	Appli
Sequence 15	Appli
Sequence 71	Appli
Sequence 71	Appli

ALIGNMENTS

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1  RESULT 1
2  US-08-218-303-16
3  ; Sequence 16, Application US/08218303
4  ; Patent No. 5547867
5  ;
6  ; GENERAL INFORMATION:
7  ; APPLICANT: Kara, Bhupendra V.
8  ; APPLICANT: Hockney, Robert C.
9  ; APPLICANT: Pitton, John E.
10 ;
11 ; TITLE OF INVENTION: FERMENTATION PROCESS
12 ;
13 ; NUMBER OF SEQUENCES: 23
14 ;
15 ; CORRESPONDENCE ADDRESS:
16 ; ADDRESSEE: Cushman, Darby & Cushman
17 ; STREET: 1615 L Street, N.W.
18 ; CITY: Washington
19 ; STATE: D.C.
20 ; COUNTRY: U.S.A.
21 ; ZIP: 20036-5601
22 ;
23 ; COMPUTER READABLE FORM:
24 ; MEDIUM TYPE: Floppy disk
25 ; COMPUTER: IBM PC Compatible
26 ; OPERATING SYSTEM: PC-DOS/MS-DOS
27 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
28 ;
29 ; CURRENT APPLICATION DATA:
30 ; APPLICATION NUMBER: US/08/218,303
31 ; FILING DATE:
32 ; CLASSIFICATION: 435
33 ;
34 ; PRIOR APPLICATION DATA:
35 ; APPLICATION NUMBER: US 07/941,533
36 ; FILING DATE: 26-FEB-1992
37 ;
38 ; ATTORNEY/AGENT INFORMATION:
39 ; NAME: Kokulis, Paul N.
40 ;
41 ; REGISTRATION NUMBER: 16,773
42 ; REFERENCE/DOCKET NUMBER: PNK/3893/94908/MJW
43 ;
44 ; TELECOMMUNICATION INFORMATION:
45 ; TELEPHONE: 202-861-3000
46 ; TELEFAX: 202-822-0944
47 ; TELEX: 6714627 CUSH
48 ;
49 ; INFORMATION FOR SEQ ID NO: 16:
50 ; SEQUENCE CHARACTERISTICS:
51 ; LENGTH: 267 amino acids
52 ; TYPE: amino acid
53 ; TOPOLOGY: linear
54 ; MOLECULE TYPE: protein
55 ;
56 ; US-08-218-303-16

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Query Match 98.4%: Score 950: DB 1: Length 267:

Best Local Similarity	94.9%	Pred. No. 1.2e-102;	0; Mismatches 0;	Indels 10; Gaps 1;
Matches 188;	Conservative			

0V 1 MVPKOYPIINFTTAGATVOSYTNFIRAVRGRLT-----VLPNRVGLPINORFILV 50

Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTGTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 2

US-08-338-793D-61
; Sequence 61, Application US/08338793D
; Patent No. 5840521
; GENERAL INFORMATION:
; APPLICANT: Barth, Peter Thomas
; TITLE OF INVENTION: VECTOR
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY CUSHMAN
; ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC/XT/AT Compatibles
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word or ASCII editors
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,793D
; FILING DATE: 08-No. 5840521-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842,081
; FILING DATE: 26-Feb-92
; CLASSIFICATION: 435
; APPLICATION NUMBER: 9104017.0
; FILING DATE: 26-Feb-91
; APPLICATION NUMBER: 9109188.4
; FILING DATE: 29-Apr-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulla, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: DJB/9901/215431/TGM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-338-793D-61

Query Match 98.4%; Score 950; DB 2; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.2e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTGTGADVRHEIPVLPNRVGLPINQRFILV 60

QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 3

US-09-538-873-1
; Sequence 1, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/09/538,873
; CURRENT FILING DATE: 2000-03-30
; EARLIER APPLICATION NUMBER: 60/126,826
; EARLIER FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-538-873-1

Query Match 98.4%; Score 950; DB 4; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.2e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTGTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFPHDPNQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 4

US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; Composition and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESS: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/901,707
 ; FILING DATE: 19920619
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5376546and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27129/30910
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-5750
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; US-07-901-707-1

Query Match 97.5%; Score 941; DB 1; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1.3e-101;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 Qy 3 PKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 3 PKQYPIINFTTAGATVQSYTNFIRAVGRGLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 Qy 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
 Db 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 122
 Qy 113 YDRLEQLAGNLRNIELGNGLPLEEASALYYVSTGGTOLPTLARSFIICIMISEAARFQ 172
 Db 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYVSTGGTOLPTLARSFIICIMISEAARFQ 182
 Qy 173 YIEGEMTRIRYNRRS 188
 Db 183 YIEGEMTRIRYNRRS 198

RESULT 5
 US-07-988-430-1
 ; Sequence 1, Application US/07988430
 ; Patent No. 5416202
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernhardt, Susan L.
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Lane, Julie A.
 ; APPLICANT: Lei, Shau-Ping
 ; TITLE OF INVENTION: Materials Comprising and Methods of
 ; Preparation and Use for Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/988,430
 ; FILING DATE: 19921209
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5416202and, Greta E.
 ; REGISTRATION NUMBER: 35302
 ; REFERENCE/DOCKET NUMBER: 31133
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; US-07-988-430-1

Query Match 97.5%; Score 941; DB 1; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1.3e-101;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 Qy 3 PKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 3 PKQYPIINFTTAGATVQSYTNFIRAVGRGLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 Qy 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
 Db 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 122
 Qy 113 YDRLEQLAGNLRNIELGNGLPLEEASALYYVSTGGTOLPTLARSFIICIMISEAARFQ 172
 Db 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYVSTGGTOLPTLARSFIICIMISEAARFQ 182
 Qy 173 YIEGEMTRIRYNRRS 188
 Db 183 YIEGEMTRIRYNRRS 198

RESULT 6
 US-08-425-336-1
 ; Sequence 1, Application US/08425336
 ; Patent No. 5621083
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; Proteins
 ; NUMBER OF SEQUENCES: 140
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFATTAGATVQSYNFIKAVRGLT-----VLPNRVGLPINORFILVEL 52
DB 3 PKQYPIINFATTAGATVQSYNFIKAVRGLTGGADVRHEIPVLPNRVGLPINORFILVEL 62
QY 53 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAFGN 112
DB 63 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAFGN 122
QY 113 YDRLEQAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFIIQMISEARFQ 172
DB 123 YDRLEQAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFIIQMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
DB 183 YIEGEMTRIRYNRRS 198

RESULT 7
US-08-488-113B-1
Sequence 1, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-1
Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFATTAGATVQSYNFIKAVRGLT-----VLPNRVGLPINORFILVEL 52
DB 3 PKQYPIINFATTAGATVQSYNFIKAVRGLTGGADVRHEIPVLPNRVGLPINORFILVEL 62
QY 53 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAFGN 112
DB 63 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAFGN 122
QY 113 YDRLEQAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFIIQMISEARFQ 172
DB 123 YDRLEQAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFIIQMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
DB 183 YIEGEMTRIRYNRRS 198
RESULT 8
US-08-477-484B-1
Sequence 1, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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QY 113 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 172
DB 123 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
DB 183 YIEGEMTRIRYNRRS 198

RESULT 9
US-08-646-360-1

;; Sequence 1, Application US/08646360
;; Patent No. 5837491
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-646-360-1
Query Match 97.5%; Score 941; DB 2; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYFAFGGN 112
DB 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYFAFGGN 122
QY 113 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 172
DB 123 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188


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Db 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
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QY 113 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
Db 123 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198

RESULT 12
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-1
Query Match 97.5%; Score 941; DB 4; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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Db 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 122
QY 113 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
Db 123 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198
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RESULT 13
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell,
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-09487-1

Query Match 97.5%; Score 941; DB 5; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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QY 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQVRYTFAFGN 112
Db 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQVRYTFAFGN 122

QY 113 YDRLEQAGNLRNLELNGPGLPEEASALYYSTGGTOLPTLARSFICIQMISEAARFQ 172
Db 123 YDRLEQAGNLRNLELNGPGLPEEASALYYSTGGTOLPTLARSFICIQMISEAARFQ 182

QY 173 YIEGEMTRIRYNRRS 188
Db 183 YIEGEMTRIRYNRRS 198

RESULT 14
US-08-356-786-8
Sequence 8, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-8

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Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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QY 173 YIEGEMTRIRYNRRS 188
Db 184 YIEGEMTRIRYNRRS 199

RESULT 15
US-08-378-761A-27
Sequence 27, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-27

Query Match 97.5%; Score 941; DB 1; Length 290;
Best Local Similarity 94.9%; Pred. No. 1.5e-101;
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QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
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147 YDRLEQLAGNLRNIELGNGLPEEAISALYYYSTGGTQLPTLARSFIIICIMISEAARFQ 206
QY 173 YIEGEMRTRIRYNRS 188
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Search completed: February 10, 2004, 16:29:33
Job time : 10.8703 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 24.2491 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

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Searched: 801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	956	99.1	190	12	US-10-083-336A-11
5	950	98.4	198	12	US-10-083-336A-7
6	950	98.4	267	12	US-10-282-935-1
7	950	98.4	267	12	US-10-440-796-1
8	941	97.5	198	12	US-10-083-336A-3
9	941	97.5	199	12	US-10-083-336A-5
10	941	97.5	200	12	US-10-083-336A-10
11	941	97.5	267	12	US-10-127-890-1
12	941	97.5	576	12	US-10-083-336A-1
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15	336	34.8	247	10	US-09-792-793A-39

16	336	34.8	247	12	US-10-127-890-6	Sequence 6, Appli
17	336	34.8	247	12	US-10-375-209A-39	Sequence 39, Appli
18	336	34.8	289	12	US-10-280-679B-4	Sequence 4, Appli
19	305	31.6	247	10	US-09-792-793A-34	Sequence 34, Appli
20	305	31.6	247	12	US-10-375-209A-34	Sequence 34, Appli
21	297.5	30.8	251	12	US-10-282-935-3	Sequence 3, Appli
22	297.5	30.8	251	12	US-10-440-796-3	Sequence 3, Appli
23	273	28.3	263	12	US-10-127-890-7	Sequence 7, Appli
24	272	28.2	263	12	US-10-127-890-4	Sequence 4, Appli
25	257.5	26.7	248	12	US-10-127-890-5	Sequence 5, Appli
26	254	26.3	252	9	US-09-347-064-2	Sequence 2, Appli
27	254	26.3	252	9	US-09-347-064-8	Sequence 8, Appli
28	245.5	25.4	251	12	US-10-127-890-107	Sequence 107, App
29	244.5	25.3	251	12	US-10-127-890-106	Sequence 106, App
30	244.5	25.3	251	12	US-10-127-890-110	Sequence 110, App
31	244.5	25.3	251	12	US-10-127-890-111	Sequence 111, App
32	243.5	25.2	251	9	US-09-765-527-247	Sequence 247, App
33	243.5	25.2	251	12	US-10-127-890-2	Sequence 2, Appli
34	243.5	25.2	251	12	US-10-127-890-99	Sequence 99, Appli
35	243.5	25.2	251	12	US-10-127-890-100	Sequence 100, App
36	243.5	25.2	251	12	US-10-127-890-101	Sequence 101, App
37	243.5	25.2	251	12	US-10-127-890-102	Sequence 102, App
38	243.5	25.2	251	12	US-10-127-890-103	Sequence 103, App
39	243.5	25.2	251	12	US-10-127-890-104	Sequence 104, App
40	243.5	25.2	251	12	US-10-127-890-105	Sequence 105, App
41	243.5	25.2	316	12	US-10-074-596-1	Sequence 1, Appli
42	243.5	25.2	507	12	US-10-074-596-11	Sequence 11, Appli
43	242.5	25.1	251	12	US-10-127-890-109	Sequence 109, App
44	242.5	25.1	293	9	US-09-765-527-259	Sequence 259, App
45	242.5	25.1	309	9	US-09-765-527-253	Sequence 253, App

ALIGNMENTS

RESULT 1
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannenmacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match	100.0%;	Score	965;	DB	12;	Length	188;
Best Local Similarity	100.0%;	Pred. NO.	1.1e-102;				
Matches	188;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MVPKQYPIINFTTAGATVQS	YTFIRAVRGRLTVLPNVRGLPINQRFILVLSNHAELSV	60			
Db	1	MVPKQYPIINFTTAGATVQS	YTFIRAVRGRLTVLPNVRGLPINQRFILVLSNHAELSV	60			
Qy	61	TLALDVTNAYVGVYAGNSAYFFHPDQEDAEATHLFTDVQNYRTTFAFGNYDRLEQLA	120				
Db	61	TLALDVTNAYVGVYAGNSAYFFHPDQEDAEATHLFTDVQNYRTTFAFGNYDRLEQLA	120				
Qy	121	GNLRNTELGNGPLEEIAISALYYSTGCTQLPTLARSFIICIMISEARFQYIEGEMRT	180				
Db	121	GNLRNTELGNGPLEEIAISALYYSTGCTQLPTLARSFIICIMISEARFQYIEGEMRT	180				
Qy	181	RIRYNRS	188				

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Db 181 RYNNRS 188
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RESULT 2
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4
Query Match 99.1%; Score 956; DB 12; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
QY 183 RYNNRS 188
Db 183 RYNNRS 188
RESULT 3
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6
Query Match 99.1%; Score 956; DB 12; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
QY 183 RYNNRS 188
Db 183 RYNNRS 188
RESULT 4
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11
Query Match 99.1%; Score 956; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
QY 183 RYNNRS 188
Db 183 RYNNRS 188
RESULT 5
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7
Query Match 99.1%; Score 956; DB 12; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
QY 183 RYNNRS 188
Db 183 RYNNRS 188
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Db 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 63
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 64 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 123
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 124 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 183
QY 183 RYNNRS 188
Db 184 RYNNRS 189
RESULT 6
US-10-083-336A-12
; Sequence 12, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-12
Query Match 99.1%; Score 956; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 64 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 123
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 124 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 183
QY 183 RYNNRS 188
Db 184 RYNNRS 189
RESULT 7
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8
Query Match 99.1%; Score 956; DB 12; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSRTL 62
QY 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 122
Db 64 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAPGGNYDRLEQLAGN 123
QY 123 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 182
Db 124 LRENIELGNGLPLEEASALYYSTGTQPTLARSFIIICQMISEAARFOYIEGEMRTRI 183
QY 183 RYNNRS 188
Db 184 RYNNRS 189
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; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match      98.4%; Score 950; DB 12; Length 198;
Best Local Similarity 94.9%; Pred. No. 6.4e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINQRFILV 60

QY 51 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 110
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 120

QY 111 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 170
Db 121 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 180

QY 171 FOYIEGEMTRIRYNRS 188
Db 181 FOYIEGEMTRIRYNRS 198

RESULT 6
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: US/282-935
; CURRENT APPLICATION NUMBER: 2002-10-29
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-282-935-1

Query Match      98.4%; Score 950; DB 12; Length 267;
Best Local Similarity 94.9%; Pred. No. 9.8e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINQRFILV 60

QY 51 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 110
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 120

QY 111 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 170
Db 121 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 180

QY 171 FOYIEGEMTRIRYNRS 188
Db 181 FOYIEGEMTRIRYNRS 198

US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3
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; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

Query Match          97.5%; Score 941; DB 12; Length 198;
Best Local Similarity 94.9%; Pred. No. 7e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
   |||||
Db 3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVHREIPVLPNRVGLPINQRFILVEL 62

QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 112
   |||||
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 122

QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 172
   |||||
Db 123 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 182

QY 173 YIEGEMTRIRYNRRS 188
   |||||
Db 183 YIEGEMTRIRYNRRS 198

RESULT 9
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-5

Query Match          97.5%; Score 941; DB 12; Length 199;
Best Local Similarity 94.9%; Pred. No. 7e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
   |||||
Db 4 PKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVHREIPVLPNRVGLPINQRFILVEL 63

QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 112
   |||||
Db 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 123

QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 172
   |||||
Db 124 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 183

QY 173 YIEGEMTRIRYNRRS 188
   |||||
Db 184 YIEGEMTRIRYNRRS 199

RESULT 10
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

Query Match          97.5%; Score 941; DB 12; Length 200;
Best Local Similarity 94.9%; Pred. No. 7e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
   |||||
Db 4 PKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVHREIPVLPNRVGLPINQRFILVEL 63

QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 112
   |||||
Db 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFGN 123

QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 172
   |||||
Db 124 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 183

QY 173 YIEGEMTRIRYNRRS 188
   |||||
Db 184 YIEGEMTRIRYNRRS 199

RESULT 11
US-10-127-890-1
; Sequence 1, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
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; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1

Query Match      97.5%; Score 941; DB 12; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.1e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVREIPIVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGCGN 112
DB 63 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGCGN 122
QY 113 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 172
DB 123 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
DB 183 YIEGEMTRIRYNRRS 198

RESULT 12
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match      97.5%; Score 941; DB 12; Length 576;
Best Local Similarity 94.9%; Pred. No. 3.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVREIPIVLPNRVGLPINQRFILVEL 97
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGCGN 112
DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGCGN 157
QY 113 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 172
DB 123 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 182

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DB 158 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 217
QY 173 YIEGEMTRIRYNRRS 188
DB 218 YIEGEMTRIRYNRRS 233

RESULT 13
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match      96.3%; Score 929.5; DB 12; Length 185;
Best Local Similarity 98.4%; Pred. No. 1.3e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTLPNRVGLPINQRFILVELSNHAELSVTL 62
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSVTL 59
QY 63 ALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGNYDRLEQLAGN 122
DB 60 ALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGNYDRLEQLAGN 119
QY 123 LRENIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQYIEGEMTRIRI 182
DB 120 LRENIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQYIEGEMTRIRI 179
QY 183 RYNRRS 188
DB 180 RYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match      69.3%; Score 669; DB 12; Length 179;
Best Local Similarity 93.0%; Pred. No. 1.1e-68;
Matches 132; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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Qy	3	PKQYDIIINFTTAGATVQSYTNFIKAVRGRLT-----VLPNRVGVLPIINORFTLVSL	52
Db	38	PKQYDIIINFTTAGATVQSYTNFIKAVRGRLTGADVHEIPVLPNRVGVLPIINORFTLVSL	97
Qy	53	SNHAELSVTLALDVTNNAVYVGYRAGNSAYFFHPDQEDABAI ¹ THLFTDVQNRVYTFAGGN	112
Db	98	SNHAELSVTLALDVTNNAVYVGYRAGNSAYFFHPDQEDABAI ¹ THLFTDVQNRVYTFAGGN	157
Qy	113	YDRLEQLAGNLRENIEILNGPL	134
Db	158	YDRLEQLAGNLRENIEILNGPL	179

RESULT, T 15

K250L1 15
 US-09-792-793A-39
 ; Sequence 39, Application US/09792793A
 ; Patent No. US20020168370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; APPLICANT: Cogghins, Philip
 ; TITLE OF INVENTION: METHODS
 ; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 ; FILE REFERENCE: 25020-601D
 ; CURRENT APPLICATION NUMBER: US/09/792,793A
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 39
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Trichosantheus kirilowii
 US-09-792-793A-39

Query Match 34.8%; Score 336; DB 10; Length 247;
Best Local Similarity 38.9%; Pred. No. 3.6e-30;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

QY	9	INFTTAGATVQSYNFRVAVRGRUTVLPN-----RVGLPINQRFILVELSNHAEL	58
Db	2	VSFRLSGATSSSYGVFFISNLR---KALPNERKLYDIPLLRASSLPQSQRVALIHLTNVADE	58
QY	59	SVTLALDVTNAAVVVGYRAGNSAYSEFHPDNOEDA-EAITHLFTDVQNYRYFAGGNVDRL	117
Db	59	TISVAIDVTNVIIMGYRAGDTSYFF---NEASATEAKYVFKDAMRKVTLPSYGNRYELQ	115
QY	118	QLAGNLRNIEILGNCPLEEAISALYYVYSTGTQTLPLARSFIICIMISEAARFQVIEGE	177
Db	116	TAAGKIRENIPGLPALDSAITLIFYNNAN-----SPAASALMVLIQSTSEARARYFIEQ	170
QY	178	MRTRI	182
Db		:	
Db	171	IGKRV	175

Search completed: February 10, 2004, 16:53:54
Job time : 25.2491 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.1735 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MWPQYPIINFTAGATVQS.....ARFOYIEGMRTIRYNRS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94.1	97.5	576	1 RLCSA	ricin D precursor
2	85.1	88.2	564	1 RLCSAG	agglutinin precursor
3	33.6	34.8	289	1 RLCSA	RNA N-glycosidase
4	327.5	33.9	528	2 S32431	abrin-d precursor
5	327.5	33.9	562	2 S16022	abrin-c precursor
6	326	33.8	247	2 JU0393	karasurin - Mongol
7	326	33.8	247	2 JU0393	karasurin-B - Tric
8	326	33.8	289	2 JU0393	karasurin C - Tric
9	323	33.5	527	2 S32430	abrin-b precursor
10	310.5	32.2	251	2 S39761	abrin (clone 7.2)
11	303.5	31.5	528	1 T2LSA	abrin-a precursor
12	300.5	31.1	278	2 S23519	beta-luffin - smoo
13	293.5	30.4	250	2 JU0108	luffin-b - smoo
14	274.5	28.4	277	2 S22494	RNA N-glycosidase
15	274	28.4	286	2 S25560	RNA N-glycosidase
16	273	28.3	286	1 RLPUFG	RNA N-glycosidase
17	273	28.3	570	2 S62627	agglutinin I precursor
18	270	28.0	245	2 JU0480	RNA N-glycosidase
19	267	27.7	285	2 JU04235	RNA N-glycosidase
20	264	27.4	254	2 JU0018	mistletoe lectin I
21	243.5	25.2	316	2 JU0753	RNA N-glycosidase
22	186.5	19.3	294	2 S28421	RNA N-glycosidase
23	174	18.0	278	2 A39817	RNA N-glycosidase
24	170	17.6	313	2 S17757	RNA N-glycosidase
25	168.5	17.5	261	2 JU0401	antiviral protein
26	148.5	15.4	289	2 T12573	RNA N-glycosidase
27	138	14.3	272	2 JU4811	betavulgin - beet
28	131	13.6	253	2 S28542	RNA N-glycosidase
29	127	13.2	253	2 S28539	RNA N-glycosidase

ALIGNMENTS

RESULT 1

RLCSA

ricin D precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <HAL>
A:Cross-references: GB:X03179; NID:G21082; PIDN:CAA26939.1; PID:G21083
R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene.
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <TRE>
A:Cross-references: EMBL:X52908; NID:G21084; PIDN:CAA37095.1; PID:G21085
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for prepro-ricin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, D', 77-550, R', 552-576 <LAM>
A:Cross-references: GB:X02388; NID:G21077; PIDN:CAA26230.1; PID:G21078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile ch
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97, Q', 99-109, S', 111-269, D', 272-283, L', 285-288, 290-302 <YOS>
A:Note: this paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, PS', 386-576 <ARA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein

30 127 13.2 253 2 S29931 rRNA N-glycosidase
31 124 12.8 283 2 S05205 rRNA N-glycosidase
32 123 12.7 253 2 S28541 rRNA N-glycosidase
33 122 12.6 310 2 S46239 ribosome-inactivat
34 121 12.5 292 1 RLQHG2 rRNA N-glycosidase
35 116.5 12.1 293 2 S17519 rRNA N-glycosidase
36 116 12.0 275 2 S33631 tritin - wheat
37 115 11.9 253 2 A58923 rRNA N-glycosidase
38 114 11.8 280 1 RLHBH rRNA N-glycosidase
39 112 11.6 280 2 JC5848 protein synthesis
40 110 11.4 236 2 S17932 rRNA N-glycosidase
41 109 11.3 319 2 S21940 hypothetical prote
42 108 11.2 319 2 I54695 shiga-like toxin I
43 108 11.2 319 2 E90779 shiga toxin 2 subu
44 108 11.2 319 2 G85640 shiga toxin 2 subu
45 107.5 11.1 318 2 S01032 shiga-like toxin I

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',405-427,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
 A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.
 A;Reference number: A48237; PMID:91352006; PMID:1881883
 A;Contents: annotation: active site
 R;Robertus, J.D.
 Proteins 10, 260-269, 1991
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
 A;Reference number: A48238; PMID:91352005; PMID:1881882
 A;Contents: annotation: X-ray crystallography, 2.5 angstroms
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
 Proteins 10, 251-259, 1991
 A;Title: Structure of ricin A-chain at 2.5 angstroms.
 A;Reference number: A48239; PMID:91352004; PMID:1881881
 A;Contents: annotation: X-ray crystallography, 2.5 angstroms
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination (lectin).
 C;Comment: This protein is cytotoxic and very poisonous to animals.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-35/Domain: signal sequence #status predicted <SIG>
 F;36-293/Domain: rRNA N-glycosidase homology <RNG>
 F;315-576/Product: ricin D chain B #status experimental <BCH>
 F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
 F;45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;212/Active site: Glu #status experimental
 F;215/Active site: Arg #status predicted
 F;294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
 F;336,349,360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental
 F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
 Query Match 97.5%; Score 941; DB 1; Length 576;
 Best Local Similarity 94.9%; Pred. No. 1.8e-76;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFNTAGATVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFNTAGATVQSYNFIKAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAEISVTLALDVNNAVYVYGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 112
 DB 98 SNHAEISVTLALDVNNAVYVYGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 157
 QY 113 YDRLEQLAGNLRENIELNGPGLPEEAISALYYSTGGTQLPTLARSFFICIQMISEARFQ 172
 DB 158 YDRLEQLAGNLRENIELNGPGLPEEAISALYYSTGGTQLPTLARSFFICIQMISEARFQ 217
 QY 173 YIEGEMTRIRYNRRS 188
 DB 218 YIEGEMTRIRYNRRS 233
 RESULT 2
 RLCSAG
 agglutinin precursor - castor bean
 N;Contents: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Ricinus communis (castor bean)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A24261
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
 J. Biol. Chem. 260, 15682-15686, 1985
 A;Title: The primary structure of Ricinus communis agglutinin. Comparison with ricin.
 A;Reference number: A24261; PMID:86059449; PMID:2999130
 A;Accession: A24261
 A;Molecule type: mRNA
 A;Residues: 1-564 <ROB>
 A;Cross-references: GB:M12089; NID:G169700; PIDN:AAA33869.1; PID:G169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
 Biochim. Biophys. Acta 872, 277-285, 1986
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 A;Reference number: A24210
 A;Accession: A24210
 A;Molecule type: protein
 A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-555,'E',557-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared with ricin.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-290/Product: agglutinin chain A #status predicted <ACH>
 F;35-281/Domain: rRNA N-glycosidase homology <RNG>
 F;303-564/Product: agglutinin chain B #status experimental <BCH>
 F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
 F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;200,203/Active site: Glu, Arg #status predicted
 F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
 F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted
 F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
 Query Match 88.2%; Score 851.5; DB 1; Length 564;
 Best Local Similarity 86.7%; Pred. No. 2.9e-70;
 Matches 170; Conservative 7; Mismatches 8; Indels 11; Gaps 2;
 QY 3 PKQYPIINFNTAGATVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 27 PKQYPIINFNTAGATVQSYNFIKAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 86
 QY 53 SNHAEISVTLALDVNNAVYVYGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 112
 DB 87 SNHAEISVTLALDVNNAVYVYGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 146
 QY 113 YDRLEQLAGNLRENIELNGPGLPEEAISALYYSTGGTQLPTLARSFFICIQMISEARFQ 172
 DB 147 YDRLEQLAGNLRENIELNGPGLPEEAISALYYSTGGTQLPTLARSFFICIQMISEARFQ 205
 QY 173 YIEGEMTRIRYNRRS 188
 DB 206 YIEGEMTRIRYNRRS 221
 RESULT 3
 RLRTZT
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake
 N;Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C;Species: Trichosanthin kirilowii (Mongolian snake-gourd)
 C;Date: 30-Sep-1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001
 C;Accession: JT0566; A36274; JCI093; A36273; JT0003
 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
 Gene 97, 267-272, 1991
 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
 A;Reference number: JT0566; PMID:91153657; PMID:1999291
 A;Accession: JT0566
 A;Molecule type: mRNA
 A;Residues: 1-289 <SHA>
 A;Cross-references: GB:M34858; NID:G170536; PIDN:AAA34207.1; PID:G170537
 R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
 J. Biol. Chem. 265, 8670-8674, 1990
 A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.
 A;Reference number: A36274; PMID:90256790; PMID:2341400
 A;Accession: A36274
 A;Molecule type: DNA
 A;Residues: 1-233,'T',235-246,'M',248-289 <CHO>
 A;Cross-references: GB:J05434; NID:G170534; PIDN:AAA34206.1; PID:G170535
 R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
 Acta Genet. Sin. 21, 42-51, 1994
 A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
 A;Reference number: JCI093; PMID:94271613; PMID:8003348
 A;Accession: JCI093

A:Molecule type: DNA
A:Residues: 1-72, 'V' 74-90, 'S' 92-233, 'T' 235-267, 'D' 269-289 <ZHE>
A:Cross-references: GB:S70176; NID:9547148; PID:9547149
R:Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
J. Biol. Chem. 265, 8665-8669, 1990
A:Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for ab
A:Reference number: A36273; MUID:90256789; PMID:2341399
A:Accession: A36273
A:Molecule type: protein
A:Residues: 24-270 <COL>
R:Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A:Title: Scientific evaluation of Tian Hua Fen (THEF): history, chemistry and application
A:Reference number: JT0003
A:Accession: JT0003
A:Molecule type: protein
A:Residues: 24-56, 'L' 58-59, 'I' 61-71, 'I' 73-81, 85-86, 'L' 88-92, 'DAGLPRAVL' 93-142, 'GL'
A:Experimental source: tuber
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A:Reference number: A67091; PDB:1MRJ
A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A:Reference number: A67092; PDB:1MRK
A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, December 1994
A:Reference number: A66711; PDB:1TCS
A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
Nat. Struct. Biol. 1, 695-700, 1994
A:Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A:Reference number: A58622; MUID:95360714; PMID:7634073
A:Contents: annotation; X-ray crystallography, 1.7 angstroms
C:Comment: Alpha-trichosanthin has been used to induce abortions.
C:Genetics:
A:Gene: tcs
C:Function:
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA thez
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient; glycosidase; hydrolase; root; toxin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-270/Product: trichosanthin alpha #status experimental <MAT>
F:27-266/Domain: rRNA N-glycosidase homology <RNG>
F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 34.8%; Score 336; DB 1; Length 289;
Best Local Similarity 38.9%; Pred. No. 2.6e-23;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

Qy 9 INFATTAGTQSYTNFIRAVRGLTTLVLPN-----RVGLPINQRFILVELSNHAE 58
Db 25 VSFLSGATSSSYGVFFISNLR---KALPNERKLYDIPILRSLSPLGSGQRYALIHLYTNVADE 81

Qy 59 SVTLALDVTNAYVVGVRAGNSAYFFHPDQDAEALHTLFTDQVNRVTFAGGNYDRL 117
Db 82 TISVAIDVTNVIYNGVRAGDSYFF---NEASATEAKYVFDAMRKVTLPSYNGYERLQ 138

Qy 118 QLAGNLRENIELNGPLEEALISALYYSTGTQTLPLARSFIIQIMISEAARFQYIEGE 177
Db 139 TAAGKIRENIPGLPALDSALTLLFYNNAN-----SAASALMWLIQSTSEAAKYKFTIEQQ 193

Qy 178 MRTRI 182
Db 194 IGKRV 198

RESULT 4
S32431
A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA39202.1; PID:g16085
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
A:Title: Precursor - Indian licorice (fragment)
C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating

C:Species: Abrus precatorius (Indian licorice)
C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C:Accession: S32431; S34408
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isoabrin determined by cDNA sequencing. Cor
A:Reference number: S32429; MUID:95132798; PMID:8421313
A:Accession: S32431
A:Molecule type: mRNA
A:Residues: 1-169, 'C' 171-320, 'L' 322-528 <HU2>
A:Cross-references: GB:M98346
R:Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-169, 'C' 171-320, 'L' 322-528 <HU2>
A:Cross-references: GB:M98346
C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
The A and B chains are linked by a single disulfide bond, which is essential for toxicit
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
F:1-251/Product: abrin-d chain A #status predicted <ACH>
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
F:261-528/Product: abrin-d chain B #status predicted <ACH>
F:283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F:174,113,195,196/Binding site: pyrrolidone carboxylic acid (Gln) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
F:200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F:288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F:500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 33.9%; Score 327.5; DB 2; Length 528;
Best Local Similarity 43.9%; Pred. No. 3.3e-22;
Matches 82; Conservative 22; Mismatches 68; Indels 15; Gaps 4;

Qy 5 QYPIIFTAGTQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVELSNHA 56
Db 1 QDQVIFTEGATSSQSYKQFIEALRQLTGLIHDPVLPDPTTVEERNYITVELSNSE 60

Qy 57 ELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEALHTLFTDQVNRVTFAGGNYDRL 116
Db 61 RESIEVGIDVTNAYVAVRAGSOSYFL---RDPASASTYLFPGTQ-RYSIRFDGSGDL 116

Qy 117 EQLAGNLRENIELNGPLEEALISALYYSTGTQTLPLARSFIIQIMISEAARFQYIEG 176
Db 117 ERWAHQTRREISLGLQALTAHS---FLRSGASNDKARTLIVIQMASEAARYISN 173

Qy 177 EMRTIR 183
Db 174 RVGVSR 180

RESULT 5
S16022
A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA39202.1; PID:g16085
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
A:Title: Precursor - Indian licorice
C:Species: Abrus precatorius (Indian licorice)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C:Accession: S16022
R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
Eur. J. Biochem. 198, 723-732, 1991
A:Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chain
A:Reference number: S16022; MUID:91266957; PMID:2050149
A:Accession: S16022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <WOO>
A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA39202.1; PID:g16085
C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
The A and B chains are linked by a single disulfide bond, which is essential for toxicit


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Query Match      33.8%; Score 326; DB 2; Length 247;
Best Local Similarity 39.6%; Pred. No. 1.7e-22;
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

QY 9 INPTTAGATVQSYTNFIRAVR-----GRITVLP-IRVGLPINORFTLVLSNHAELSVT 61
Db 2 VSEFLSGATSSSCYGFISNRKALPKALPKERKYLDIPLEIRSLTPGGRVALIHLLTINVADETTIS 61

QY 62 LAIDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRYYTFAFGNYDRLEQLA 120
Db 62 VALDVTNVVYMGYRAGDTSYFF--NEASATEAAKYVFKDKRKVTLPYSGNYERLQIAA 118

QY 121 GNLRNELTNGPLGEAISALYXYSTGGTQLPTLARSFIICIMISEAARFQVEGEMPT 180
Db 119 GKIRENPLGLPALDSAITTLFYNN-----SAASALMVLIOSTSEARKYFTEQOIGK 173

QY 181 RI 182
Db 174 RV 175

```

Query Match 33.8%; Score 326; DB 2; Length 289;
Best Local Similarity 39.6%; Pred. No. 2.1e-22;
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

Dd 173 RVGVSIRTN 181

RESULT 10
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: C39761; S14471
R:Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A:Title: Direct molecular cloning and expression of two distinct abrin A-chains
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Accession: C39761
A:Molecule type: DNA
A:Residues: 1-251 <EVE>
R:Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A:Description: Direct molecular cloning of two distinct abrin A-chains.
A:Reference number: S14471
A:Accession: S14471
A:Molecule type: DNA
A:Residues: 'M', 1-251 <EV2>
A:CROSS-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted

Query Match 32.2%; Score 310.5; DB 2; Length 251;
Best Local Similarity 43.2%; Pred. No. 4.7e-21;
Matches 79; Conservative 22; Mismatches 67; Indels 15; Gaps 4;

Qy 9 INPTTAGATVQSNTNFIRAVGRLL-----TVLPNRVGCLPINORFILVELSNHAELSV 60
Db ||||| ||||| ||||| : : : : :
5 IKFTSGATSSQSKYKQTEALRELRGLTHDIPVLRLDPTTVEERNRYITVELSNSERESI 64

Qy 61 TLIALDVTAIVVGYRAGNSAYFFHPDNQDEDAIHTFLTDVQNRYTFAGGNYDLQLA 120
Db ||||| ||||| ||||| : : : : :
65 EVGIDVTNAVVAIRAGSOSYFL---RDAPASASTYLTGTQC-RYSLRFDSYGDLERWA 120

Qy 121 GNLRNIENLGNGFLBEAIISALYYSTGGTQTPLARSFTICIMISEARFOYIEGMRT 180
Db ||||| ||||| ||||| : : : : :
121 HQTRQISLGLQALTHAIS--FLRSASNDKEAKRTLIIVIQMASEARYEYISNRGV 177

Qy 181 RIR 183
Db |||||
178 SIR 180

RESULT 11
TZLSA
abrin-a precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C:Accession: S32429; J70202; A39761; JC1398; S14472; S24133; S74110; S74111
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isoabrins determined by cDNA sequencing
A:Reference number: S32429; MUID:93132798; PMID:8421313
A:Accession: S32429
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'E', 2-528 <HUN>
A:CROSS-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A>Note: the coding region for the sequence shown is preceded by an ATG codon
A>Note: residues 1-8 were derived from the synthesized primer
R:Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988


```

Best Local Similarity 33.7%; Pred. No. 1.7e-19;
Matches 63; Conservative 46; Mismatches 57; Indels 21; Gaps 4;

QY 9 INFTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINORFILVELSNHAEL 58
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 3 VSFSLSGADSKSYKFTALRKALPSKEKYSNIPLLPSSAGA---SRYLMLQSLNDYAK 59
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 59 SVTLALDVNTAVYGVYRAGNSAYFEHPDNOBDAEATHLFTDQVQRVTFAPGGNYDRLEQ 118
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 AITWALDVNTVYINGVLVNSTSYF---ANESDKLASQVYFKGSTLVTPYSGNYERLQN 116
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 119 LAGNLRNIELNGPLEEAISALVYVSTGGTQLTFLARSFLICCIOMISEAARFOYIEGM 178
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 117 AAGKIREKPIGLFRALDSALTSIFHYDS-----TAAAAAFVLVILQTTAAASRFKYIEGQI 171
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 179 RTRIRYN 185
   |||
Db 172 IERIPKN 178
   |||

RESULT 14
S22494
rRNA N-glycosidase (BC 3.2.2.22) alpha-luffin precursor - smooth loofah
N/Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A
C/Species: Luffia cylindrica (smooth loofah)
C/Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 20-Aug-1999
C/Accession: S22494; S26390; JH0202; A32542
R/Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 18, 1199-1202, 1992
A/Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein
A/Reference number: S22494; MUID:92288316; PMID:1600156
A/Accession: S22494
A/Molecule type: mRNA
A/Residues: 1-277 <KAT>
A/Cross-references: EMBL:XG2371; NID:g19145; PIDN:CAA44229.1; PID:g19146
R/Islam, M.R.; Nishida, H.; Funatsu, G.
Agric. Biol. Chem. 54, 2967-2978, 1990
A/Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
A/Reference number: S26390; MUID:91248471; PMID:1368651
A/Accession: S26390
A/Molecule type: protein
A/Residues: 21-53,'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL'
R/Islam, M.R.; Nishida, H.; Funatsu, G.
Agric. Biol. Chem. 54, 1343-1345, 1990
A/Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
A/Reference number: JH0202; MUID:91197482; PMID:1368623
A/Accession: JH0202
A/Molecule type: protein
A/Residues: 21-53,'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL'
A/Experimental source: seed
R/Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J.
Biochem. Biophys. Res. Commun. 160, 509-516, 1989
A/Title: Characterization of a translation inhibitory protein from Luffa aegyptiaca.
A/Reference number: A32542; MUID:89246493; PMID:2719679
A/Accession: A32542
A/Status: preliminary
A/Molecule type: protein
A/Residues: 21-28,'G',30,'X',32-34,'K',36-40 <RAM>
C/Function:
A/Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: glycoprotein; glycosidase; hydrolase; seed; toxin
F/I-20/Domain: signal sequence #status predicted <SIG>
F/I-267/Product: rRNA N-glycosidase alpha-luffin #status experimental <MAT>
F/I-262/Domain: rRNA N-glycosidase homology <RNG>
F/I-268-277/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F/I-48,53,97,104,225,246/Binding site: carboxylate (Asn) (covalent) #status experimental
F/I-90,179,182/Active site: Tyr, Glu, Arg #status predicted

Query Match 28.4%; Score 274.5; DB 2; Length 277;
Best Local Similarity 33.3%; Pred. No. 1.1e-17;
Matches 63; Conservative 42; Mismatches 61; Indels 23; Gaps 5;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55 ; Search time 6.27131 Seconds
(without alignments)
1409.756 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVPKQYPIINFATAGTQVS.....ARFQVIEGEMRTRINRNS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	941	97.5	576	1 RICI_RICCO	P02879 ricinus com
2	851.5	88.2	564	1 AGSL_RICCO	P06750 ricinus com
3	336	34.8	289	1 RIPT_TRIKI	P09989 trichosan
4	327.5	33.9	562	1 ABRG_ABRER	P28590 abrus prec
5	326	33.8	289	1 RIPS_TRIKI	P24478 trichosan
6	323	33.5	527	1 ABRB_ABRER	Q06077 abrus prec
7	320.5	33.2	282	1 RBP2_BRYDI	P98184 bryonia dio
8	307.5	31.9	563	1 RIGB_SAMNI	P33183 sambucus ni
9	305	31.6	290	1 RBP1_BRYDI	P33185 bryonia dio
10	303.5	31.5	528	1 ABRA_ABRER	P11140 abrus prec
11	293.5	30.4	250	1 RBPB_LUFVCY	P22851 luffa cylin
12	281.5	29.2	286	1 RBP1_CUCFI	Q9FRX4 cucumis fig
13	274.5	28.4	277	1 RIPA_LUFVCY	Q00465 luffa cylin
14	274	28.4	286	1 RBP2_MOMBA	P29339 momordica b
15	273	28.3	286	1 RBP1_MOMCH	P16094 momordica c
16	264	27.4	254	1 MIA_VISAL	P18446 viscum albu
17	257	26.6	294	1 RBP1_TRIAN	P56626 trichosan
18	243.5	25.2	316	1 RBP2_GELMU	P33186 gelonium mu
19	186.5	19.3	294	1 RIPA_PHYAM	Q03464 phytolacca
20	174	18.0	278	1 RBP1_MIRBA	P21326 mirabilis j
21	170	17.6	313	1 RBP1_PHYAM	P10297 phytolacca
22	168.5	17.5	261	1 RIPS_PHYAM	P23339 phytolacca
23	131	13.6	253	1 RBP7_SAPOF	Q41391 saponaria o
24	127	13.2	253	1 RBP5_SAPOF	Q41389 saponaria o
25	124	12.8	299	1 RBP6_SAPOF	P20656 saponaria o
26	122	12.6	310	1 RBP2_PHYAM	Q40772 phytolacca
27	121	12.5	293	1 RBP2_SAPOF	P27559 saponaria o
28	116.5	12.1	293	1 RBP0_DIACA	P24476 dianthus ca
29	114	11.8	280	1 RBP2_HORVU	P04399 hordeum vul
30	110	11.4	236	1 RBP3_SAPOF	P27560 saponaria o
31	107	11.2	319	1 SUTA_BP933	P09385 bacterioph
32	107	11.1	280	1 RBP1_HORVU	P22244 hordeum vul
33	101	10.5	300	1 RBP3_MAIZE	P25891 zea mays (m

34	99	10.3	301	1 RBPX_MAIZE	P28522 zea mays (m
35	96.5	10.0	315	1 SUTA_BPH19	P08026 bacterioph
36	95.5	9.9	304	1 RBP9_MAIZE	P25892 zea mays (m
37	95.5	9.9	315	1 SUTA_BPH30	P10149 bacterioph
38	85.5	8.9	1165	1 SVV_AQUAE	O67411 aquifex aco
39	81.5	8.4	305	1 Y348_MYCPN	P75255 mycoplasma
40	79	8.2	560	1 J160_HORVU	Q00531 hordeum vul
41	78	8.1	747	1 ORPB_HUMAN	Q9Bxb4 homo sapien
42	76.5	7.9	609	1 HAPT_VIBCH	P24153 vibrio chol
43	76	7.9	157	1 RBP4_SAPOF	P27561 saponaria o
44	75.5	7.8	609	1 NRPV_VIBBR	Q00971 vibrio prot
45	75	7.8	224	1 GPH_HAEIN	P44755 haemophilus

ALIGNMENTS

RESULT 1
ID RICI_RICCO STANDARD; PRT; 576 AA.
AC P02879; P02880;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase)
DE (EC 3.2.2.22); Ricin B chain].
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3398;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86067214; PubMed=2999712;
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
RA Weaver R.F.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
RT communis.";
RL Nucleic Acids Res. 13:8019-8033 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92163016; PubMed=1371405;
RT Tregear J.W., Roberts L.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
RT ricin gene and three lectin pseudogenes.";
RL Plant Mol. Biol. 18:515-525 (1992).
RN [3]
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=3838723;
RA Lamb A., Roberts L.M., Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin.";
RL Eur. J. Biochem. 148:265-270 (1985).
RN [4]
RP SEQUENCE OF 36-302.
RA Yoshitake S., Funatsu G., Funatsu M.;
RT "Isolation and sequences of peptic peptides, and the complete
RT sequence of Ile chain of ricin-D.";
RL Agric. Biol. Chem. 42:1267-1274 (1978).
RN [5]
RP SEQUENCE OF 315-576.
RA Funatsu G., Kimura M., Funatsu M.;
RT "Primary structure of Ala chain of ricin D.";
RL Agric. Biol. Chem. 43:2221-2224 (1979).
RN [6]
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1368517;
RA Kimura Y., Kusuku H., Tada M., Takagi S., Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant.";
RL Agric. Biol. Chem. 54:157-162 (1990).
RN [7]
RP REVIEW.
RX MEDLINE=21480122; PubMed=11595634;
RA Olanes S., Kozlov J.V.;

RT "Ricin.";
 RL Toxicon 39:1723-1728 (2001).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=87165983; PubMed=3558397;
 RA Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B.,
 RA Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
 RA "The three-dimensional structure of ricin at 2.8 A.";
 RL J. Biol. Chem. 262:5398-5403 (1987).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=91352004; PubMed=1881881;
 RA Katzin B.J., Collins E.J., Robertus J.D.;
 RA "Structure of ricin A-chain at 2.5 A.";
 RL Proteins 10:251-259 (1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RX MEDLINE=91352005; PubMed=1881882;
 RA Rutenber E., Robertus J.D.;
 RA "Structure of ricin B-chain at 2.5-A resolution.";
 RL Proteins 10:260-269 (1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=95082010; PubMed=7990130;
 RA Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
 RA Paupit R.A.;
 RA "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
 RL J. Mol. Biol. 244:410-422 (1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
 RX MEDLINE=96374222; PubMed=8780513;
 RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
 RA Molina-Svinth M.C., Robertus J.D.;
 RA "Structure and activity of an active site substitution of ricin A chain.";
 RL Biochemistry 35:11098-11103 (1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=97240820; PubMed=9086280;
 RA Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
 RA Robertus J.D.;
 RA "Structure-based identification of a ricin inhibitor.";
 RL J. Mol. Biol. 266:1043-1049 (1997).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE=93165632; PubMed=1287657;
 RA Kin Y., Robertus J.D.;
 RA "Analysis of several key active site residues of ricin A chain by mutagenesis and x-ray crystallography.";
 RL Protein Eng. 5:775-779 (1992).
 CC -|- FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -|- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -|- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
 CC -|- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
 CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -|- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -|- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
 CC -|- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 31 of February 2003;
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
 CC -----
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 CC -----
 CC EMBL; X03179; CAA36939.1; -;
 CC EMBL; X52908; CAA37095.1; -;
 CC EMBL; X02388; CAA26230.1; -;
 CC EMBL; A12892; CAA01058.1; -;
 CC PIR; A24041; RUCSD.
 CC PDB; 2AA1; 31-JAN-94.
 CC PDB; 1APG; 31-JAN-94.
 CC PDB; 1FMP; 31-OCT-93.
 CC PDB; 1IFS; 14-JAN-98.
 CC PDB; 1IFT; 14-JAN-98.
 CC PDB; 1IFU; 14-JAN-98.
 CC PDB; 1RUC; 31-OCT-93.
 CC PDB; 1OBS; 16-JUN-97.
 CC PDB; 1OBT; 16-JUN-97.
 CC PDB; 1BR5; 02-SEP-98.
 CC PDB; 1BR6; 02-SEP-98.
 CC PDB; 1IL3; 16-JAN-02.
 CC PDB; 1IL4; 16-JAN-02.
 CC PDB; 1IL9; 16-JAN-02.
 CC GlycoSuiteDB; P02879; -;
 CC InterPro; IPR000772; Ricin_B_lectin.
 CC InterPro; IPR001574; RIP.
 CC Pfam; PF00652; Ricin_B_lectin; 6.
 CC Pfam; PF00461; RIP; 1.
 CC PRINTS; P00396; SHIGARICIN.
 CC SMART; SM00458; RICIN; 2.
 CC PROSITE; P850231; RICIN_B_LECTIN; 2.
 CC PROSITE; P800275; SHIGA_RICIN; 1.
 CC KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 CC Glycoprotein; Lectin; Signal; 3D-structure.
 CC SIGNAL 1 35
 CC FT CHAIN 36 302 RICIN A CHAIN.
 CC FT PEPTIDE 303 314 LINKER PEPTIDE.
 CC FT CHAIN 315 576 RICIN B CHAIN.
 CC FT DOMAIN 321 448 RICIN B-TYPE LECTIN 1.
 CC FT REPEAT 451 575 RICIN B-TYPE LECTIN 2.
 CC FT REPEAT 374 414 1-ALPHA.
 CC FT REPEAT 417 449 1-BETA.
 CC FT REPEAT 462 497 1-GAMMA.
 CC FT REPEAT 501 540 2-ALPHA.
 CC FT REPEAT 543 570 2-BETA.
 CC FT ACT SITE 212 212 2-GAMMA.
 CC FT DISULFID 294 318 INTERCHAIN.
 CC FT DISULFID 334 353
 CC FT DISULFID 377 394
 CC FT DISULFID 465 478
 CC FT DISULFID 504 521
 CC FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 271 271 /FTIC-CAR 000080.
 CC FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (IN MINOR FORM).
 CC FT CARBOHYD 449 449 /FTIC-CAR 000081.
 CC FT CARBOHYD 46 76 N-LINKED (GLCNAC. . .).
 CC FT CONFLICT 551 551 E -> D (IN REF. 3).
 CC FT CONFLICT 43 47 MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
 CC FT STRAND 49 50 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC TURN

Query Match 97.5%; Score 941; DB 1; Length 576;
 Best Local Similarity 94.9%; Pred. No. 1.5e-79;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 97

QY 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 112
 DB 98 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 157

QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFFICQMISEAARFQ 172
 DB 158 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFFICQMISEAARFQ 217

QY 173 YIEGEMTRIRYNRRS 188
 DB 218 YIEGEMTRIRYNRRS 233

RESULT 2
 AGGL_RICCO STANDARD; PRT; 564 AA.

ID AGGL_RICCO
 AC P06750;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain).
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86059449; PubMed=2999130;
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with
 RL ricin";
 RL J. Biol. Chem. 260:15682-15686 (1985).
 RN [2]
 RP SEQUENCE OF 303-564.
 RC TISSUE=Seed;
 RA Araki T., Yoshioka Y., Funatsu G.;
 RT "The complete amino acid sequence of the B-chain of the Ricinus
 RL communis agglutinin isolated from large-grain castor bean seeds.";
 RL Biochim. Biophys. Acta 872:277-285 (1986).
 RN [3]
 RP SEQUENCE OF 303-337.
 RX MEDLINE=80178723; PubMed=6768555;
 RA Lin T.-S., Li S.-L.;
 RT "Purification and physicochemical properties of ricins and
 RL agglutinins from Ricinus communis.";
 RL Eur. J. Biochem. 105:453-459 (1980).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC -----
 CC EMBL; M12089; AAA33869.1; -;
 CC EMBL; S40368; AAB22584.1; -;

DR PIR; A24261; RLCSAG.
 DR HSP; P02879; IRR6.
 DR GlycoSuiteDB; P06750; -;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin 1.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 AGGLUTININ A CHAIN.
 FT PROPEP 291 302 LINKER PEPTIDE.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 405 437 1-GAMMA.
 FT REPEAT 450 485 2-ALPHA.
 FT REPEAT 489 528 2-BETA.
 FT REPEAT 531 558 2-GAMMA.
 FT ACT SITE 200 200 BY SIMILARITY.
 FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 322 341 BY SIMILARITY.
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 362 362 N -> D (IN REF. 2).
 FT CONFLICT 374 374 R -> G (IN REF. 2).
 FT CONFLICT 404 404 R -> T (IN REF. 2).
 FT CONFLICT 552 552 F -> V (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;

Query Match 88.2%; Score 851.5; DB 1; Length 564;
 Best Local Similarity 86.7%; Pred. No. 2.8e-71;
 Matches 170; Conservative 7; Mismatches 8; Indels 11; Gaps 2;

QY 3 PKQPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 27 PKQPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 86

QY 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 112
 DB 87 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 146

QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFFICQMISEAARFQ 172
 DB 147 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFFICQMISEAARFQ 205

QY 173 YIEGEMTRIRYNRRS 188
 DB 206 YIEGEMTRIRYNRRS 221

RESULT 3
 RIPT_TRIKI STANDARD; PRT; 289 AA.

ID RIPT_TRIKI
 AC P09989;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein alpha-trichosanthin precursor
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_taxid=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RX MEDLINE=91153657; PubMed=1999291;
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RT "Cloning of trichosanthin cDNA and its expression in *Escherichia*
 RL *coli*.";
 RL Gene 97:267-272(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Maximowicz; TISSUE=Leaf;
 RC MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;
 RX "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RT type I ribosome-inactivating protein.";
 RL J. Biol. Chem. 265:8670-8674(1990).
 RN [3]
 RN SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz; TISSUE=Tuberous root;
 RX MEDLINE=90256789; PubMed=2341399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RW Wu P., Hwang K., Piatak M.;
 RT "Primary amino acid sequence of alpha-trichosanthin and molecular
 RL models for abrin A-chain and alpha-trichosanthin.";
 RL J. Biol. Chem. 265:8665-8669(1990).
 RN [4]
 RN SEQUENCE OF 24-270.
 RC TISSUE=tuberous root;
 RW Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
 RA Tian G.Y., Ni C.Z.;
 RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
 RL application.";
 RL Pure Appl. Chem. 58:789-798(1986).
 RN [5]
 RN X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
 RT "Structure of trichosanthin at 1.88-A resolution.";
 RL Proteins 19:4-13(1994).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RL depurinatin mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M34858; AAA34207.1; --
 CC EMBL; J05434; AAA34206.1; --
 CC PIR; J05566; RLTTZ.
 CC PDB; 1MRJ; 07-FEB-95.
 CC PDB; 1MRK; 07-FEB-95.
 CC PDB; 1TCS; 10-JUL-95.
 CC PDB; 1J4G; 28-JAN-03.

DR PDB; 1NLI; 21-JAN-03.
 DR PDB; 1QD2; 24-APR-00.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT
 FT PROPEP 271 289
 FT ACT SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT TURN 205 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT TURN 263 263
 FT TURN 266 268
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;
 MISSING IN MATURE PROTEIN.
 BY SIMILARITY.
 IPLL -> GPLI (IN REF. 4).
 MISSING (IN REF. 4).
 I -> L (IN REF. 4).
 V -> VDAGLPNAVIL (IN REF. 4).
 KI -> GL (IN REF. 4).
 K -> S (IN REF. 4).
 WS -> LWL (IN REF. 4).
 Q -> T (IN REF. 4).
 S -> T (IN REF. 2).
 MISSING (IN REF. 4).
 T -> M (IN REF. 2).

Query Match 34.8%; Score 336; DB 1; Length 289;
 Best Local Similarity 38.9%; Pred. No. 6.5e-24;
 Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

